

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 13, 2003, 06:09:06 ; Search time 57 Seconds

(without alignments)
1937.658 Million cell updates/sec

Title: US-09-905-744b-6

Perfect score: 2250

Sequence: 1 MATSGTFFVFLVSVVCVCSA.....ETGHALGATFLLQLSLGISH 428

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

1: sp archaea.*

2: sp bacteria.*

3: sp fungi.*

4: sp human.*

5: sp invertebrate.*

6: sp mammal.*

7: sp mnc.*

8: sp organelle.*

9: sp phage.*

10: sp plant.*

11: sp rodent.*

12: sp virus.*

13: sp vertebrate.*

14: sp unclassified.*

15: sp rvirus.*

16: sp bacteriaph.*

17: sp archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2236	99.4	428	Q96RX0	Q96RX0 homo sapien
2	2104	93.5	407	Q8WUB3	Q8WUB3 homo sapien
3	1990.5	88.5	427	Q8CD29	Q8CD29 mus musculus
4	1984.5	88.2	427	Q8BR23	Q8BR23 mus musculus
5	996	44.3	483	Q8TAS7	Q8TAS7 homo sapien
6	996	44.3	503	Q8N3H3	Q8N3H3 homo sapien
7	696.5	31.0	461	O76268	O76268 drosophila
8	696.5	31.0	464	Q9VQ18	Q9VQ18 drosophila
9	616.5	27.4	479	Q9XU84	Q9XU84 caenorhabdi
10	593	26.4	278	Q8CH23	Q8CH23 mus musculus
11	538.5	23.9	556	Q9UT35	Q9UT35 schizosacch
12	518.5	23.0	489	Q8H7L6	Q8H7L6 oryza sativ
13	515.5	22.9	599	Q8TGH6	Q8TGH6 candida alb
14	511	22.7	522	Q9HEM6	Q9HEM6 kluyveromyc
15	507.5	22.6	455	Q9SPM6	Q9SPM6 medicago sa
16	503.5	22.4	467	Q9SPW7	Q9SPW7 dolichos bi

17	498	22.1	462	10	Q9XFC9	Q9Xfc9 dolichos bi
18	491.5	21.8	456	10	Q9SPM8	Q9spm8 lotus japon
19	489	21.7	455	10	Q9FEA6	Q9feae pisum sativ
20	489	21.7	472	10	Q8L704	Q8l704 arabidopsis
21	488	21.7	463	10	Q9FVC3	Q9fvc3 glycine soj
22	488	21.7	472	10	Q9SPM5	Q9spm5 arabidopsis
23	486	21.6	455	10	Q8GTB1	Q8gtb1 pisum sativ
24	485	21.6	472	10	Q9M7B3	Q9m7b3 arabidopsis
25	484	21.5	471	10	Q9SQG2	Q9sqg2 arabidopsis
26	481	21.4	447	10	Q9SLV4	Q9slv4 pisum sativ
27	475	21.1	468	10	Q9FVC2	Q9fvc2 glycine soj
28	473	21.0	467	10	Q8RVT6	Q8rvt6 pisum sativ
29	472	21.0	407	10	Q9AVN8	Q9avn8 pisum sativ
30	472	21.0	455	10	Q8RVU0	Q8rvu0 pisum sativ
31	465	20.7	447	10	Q9FUI1	Q9fui1 pisum sativ
32	464.5	20.6	558	3	Q8TGG8	Q8tgg8 aspergillus
33	462	20.5	466	10	Q9AUI5	Q9auis medicago tr
34	449	20.0	455	10	Q8RVT9	Q8rvt9 pisum sativ
35	443	19.7	473	10	Q8RVT8	Q8rvt8 pisum sativ
36	436.5	19.4	556	3	Q9C2M0	Q9c2m0 neurospora
37	435.5	19.4	271	5	Q8IPZ6	Q8ipz6 drosophila
38	432.5	19.2	555	10	Q94E22	Q94e22 arabidopsis
39	429.5	19.1	555	10	Q8O612	Q8o612 arabidopsis
40	424.5	18.9	224	11	Q8CDB6	Q8cdb6 mus musculu
41	397	17.6	483	10	Q9X162	Q9xi62 arabidopsis
42	392	17.4	493	13	Q90X66	Q90x66 gallus gall
43	385	17.1	690	5	Q9BHV5	Q9bhv5 leishmania
44	370	16.4	539	11	Q8CDV7	Q8cdv7 mus musculu
45	367	16.3	510	11	Q92106	Q921q6 mus musculu

ALIGNMENTS

RESULT 1

Q96RX0 PRELIMINARY; PRT; 428 AA.

AC Q96RX0; (TREMREL. 19, Created)

DT 01-DEC-2001 (TREMREL. 19, Last sequence update)

DT 01-MAR-2002 (TREMREL. 20, Last annotation update)

DE PcpH proto-oncogene protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20173601; PubMed=10708485;

RA Racio J.A.; Zambrano N., Pena, Ld, Reig J.A., Rhoads A., Rouzaut A.,

RA Notario V.;

RT "The human PCPH proto-oncogene: cDNA identification, primary

RT structure, chromosomal mapping, and expression in normal and tumor

RT cells.";

RL Mol. Carcinog. 27:229-236(2000).

DR EMBL; AF136572; AK82950.1; -

DR InterPro; IPR000407; GDAL_CD39_NTPase.

DR Pfam; PF01150; GDAL_CD39; 1.

SQ SEQUENCE 428 AA; 47431 MW; F2C4F7DE650A44F6 CRC64;

Query Match 99.4%; Score 2236; DB 4; Length 428;
Best Local Similarity 99.5%; Pred. No. 3.4e-185;
Matches 426; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATSGTFFVFLVSVVCVCSAVSHRNQQTWFGIFLSSNCPINVSASTLYGIMFAGSTGT 60

DB 1 MATSGTFFVFLVSVVCVCSAVSHRNQQTWFGIFLSSNCPINVSASTLYGIMFAGSTGT 60

QY 61 RIHVTFVQKMGQQLPILGEVFDVSKVGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

DB 61 RIHVTFVQKMGQQLPILGEVFDVSKVGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

QY 121 KPTVPVVLKATAGLRLLPEHKALLFEVKEIPFRKSPFLVPKGSVIMDGSDEGLAWTV 180

```
Db 121 KKTTPVVLKATAGLRLPEHKAKALLFEVKEIFRKSPFLVPKGSVIMDGSDEGILAWTV 180
Qy 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEKTLBOTPRGYLTSFEMFNSTYKLYTH 240
Db 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEKTLBOTPRGYLTSFEMFNSTYKLYTH 240
Qy 241 SYLGFGGLKAARLATLGALETGTGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
Db 241 SYLGFGGLKAARLATLGALETGTGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
Qy 301 EPCYAEVLRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNTETGHALGATPHL 420
Db 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNTETGHALGATPHL 420
Qy 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 2
Q8WUB3 PRELIMINARY; PRT; 407 AA.
AC Q8WUB3;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Similar to ectonucleoside triphosphate diphosphohydrolase 5.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg 8.;
RA Tissue-Colon;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020966; AAH20966.1; -.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
KW Hydrolase.
SQ SEQUENCE 407 AA; 45336 MW; D92AS7DC9EC9E5B CRC64;

Query Match 93.5%; Score 2104; DB 4; Length 407;
Best Local Similarity 100.0%; Pred. No. 8.7e-174; Mismatches 0; Indels 0; Gaps 0;
Matches 400; Conservative 0;

Qy 1 MATSWGTVPFVLMVVCVCSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSWGTVPFVLMVVCVCSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHYTTFVQKMPQLPILGEVEFDSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHYTTFVQKMPQLPILGEVEFDSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
Qy 121 KKTTPVVLKATAGLRLPEHKAKALLFEVKEIFRKSPFLVPKGSVIMDGSDEGILAWTV 180
Db 121 KKTTPVVLKATAGLRLPEHKAKALLFEVKEIFRKSPFLVPKGSVIMDGSDEGILAWTV 180
Qy 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEKTLBOTPRGYLTSFEMFNSTYKLYTH 240
Db 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEKTLBOTPRGYLTSFEMFNSTYKLYTH 240
Qy 241 SYLGFGGLKAARLATLGALETGTGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
Db 241 SYLGFGGLKAARLATLGALETGTGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
Qy 301 EPCYAEVLRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNTETGHALGATPHL 420
Db 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNTETGHALGATPHL 420
Qy 421 LQSLGISH 428
Db 421 LQSLGISH 428
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Db 301 EPCYAEVLRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQ 400
Db 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQ 400

RESULT 3
Q8CD29 PRELIMINARY; PRT; 427 AA.
AC Q8CD29;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 5.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).
DR EMBL; AK031581; BAC27461.1; -.
SQ SEQUENCE 427 AA; 47101 MW; 6E3773C842B58477 CRC64;

Query Match 88.5%; Score 1990.5; DB 11; Length 427;
Best Local Similarity 88.1%; Pred. No. 6.5e-164; Mismatches 25; Indels 1; Gaps 1;
Matches 376; Conservative 25;

Qy 1 MATSWGTVPFVLMVVCVCSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSWGTVPFVLMVVCVCSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 59
Qy 61 RIHYTTFVQKMPQLPILGEVEFDSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHYTTFVQKMPQLPILGEVEFDSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 119
Qy 121 KKTTPVVLKATAGLRLPEHKAKALLFEVKEIFRKSPFLVPKGSVIMDGSDEGILAWTV 180
Db 121 KKTTPVVLKATAGLRLPEHKAKALLFEVKEIFRKSPFLVPKGSVIMDGSDEGILAWTV 179
Qy 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEKTLBOTPRGYLTSFEMFNSTYKLYTH 240
Db 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEKTLBOTPRGYLTSFEMFNSTYKLYTH 239
Qy 241 SYLGFGGLKAARLATLGALETGTGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
Db 241 SYLGFGGLKAARLATLGALETGTGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 299
Qy 301 EPCYAEVLRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 359
Qy 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNTETGHALGATPHL 420
Db 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNTETGHALGATPHL 419
Qy 421 LQSLGISH 427
Db 421 LQSLGISH 426

RESULT 4
Q8BR23 PRELIMINARY; PRT; 427 AA.
ID Q8BR23;
AC Q8BR23;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
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QY 97 PKQAGTVOGLLEAKVDSIPRSHWKTTPVVLKATAGRLRLPEHAKALLFEVKEIRKSP 156
 DB 168 VEKSAQIGRELLOVAKQDIPDFWKAATPLVLKATAGRLRLPEHAKALLFEVKEIRKSP 227
 QY 157 FLVFKGVSINDSGDEGLAWTVNFTGQLHGHRETGTDLGGASTQITLPEFKE 216
 DB 228 FLVGDCCVSNMGDEGSAWITINFTLSTKTPGGSSVGMGLGGSTQIAFLPRVEGT 287
 QY 217 LEQTPRGYLTSEFMFNSTYKLYTHSYLGFGLKARLALATLGALETE-CTDCHTFRSACLPR 275
 DB 288 LQASPGGLTALRNFNRTYKLYSYLGLMSRLAILGVGQPAKQKQKELVSLSP 347
 QY 276 WLEAEWIPGGVYQYQGNQGEVGFEPCEYAEVLVRVKGHLHQPEVQSGSFYAFSYYYR 335
 DB 348 SFKGEWEHAEVTRYVSGKAAASLHELCAARVSEVLQNRVHRTVEVKHVDYAFSYYYDL 407
 QY 336 AVDTDMIDYKGGILKVEDFERKAREVCNLENFTSGSPFLCWDLSYITALLKDGFGPAD 395
 DB 408 AAGVGLIDAEKGGSLVGVDFEIAAKYVCTLETQPSQSPSCMDLTVVSLLLQE-FGFPR 466
 QY 396 STVLQTKKVNNTGMAFGATFHLQSL 424
 DB 467 SKVLKLTAKIDNVETSWALGAIFHYIDSL 495
 RESULT 7
 O76268 PRELIMINARY; PRT; 461 AA.
 ID O76268
 AC O76268
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DE NTPASE protein (LD11641P).
 GN NTPASE OR CG3059.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazer V.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98341119; PubMed=9676430;
 RA Chadwick S.P., Frischaut A.-M.;
 RT "The CD39-like gene family: identification of three new human members
 (CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of
 the gene family from Drosophila melanogaster";
 RL Genomics 50:357-367 (1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuncio J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003581; AAF51182.1; -
 DR EMBL; AF041048; AAC39133.1; -
 DR EMBL; AY061134; AAL28682.1; -
 DR FlyBase; FBGN0024947; NTPase.
 DR InterPro; IPR000407; GDAI_CD39_NTPase.
 DR Pfam; PF01150; GDAI_CD39; 1.
 SQ SEQUENCE 461 AA; 50845 MW; 27D00321F91A9DD1 CRC64;
 Query Match 31.0%; Score 696.5; DB 5; Length 461;
 Best Local Similarity 39.1%; Pred. No. 1.1e-51;
 Matches 156; Conservative 74; Mismatches 122; Indels 47; Gaps 12;
 QY 49 YGIMFDAGSTGTRIHHVTVFVKQPGOLPILEGEVDSVKPGLSAFVDPKQGAETVQGLL 108
 DB 79 YAAIIDAGSTGSRVLAAYKFNRSFDINKLVLYEELFKERKGLSFDADNPAEGHISIKLL 138
 QY 109 EVAKDSIPRSHWKTTPVVLKATAGRLRLPEHAKALLFEVKEIRKSPFLVPGKVSIND 168
 DB 139 DEARAFIPKEHWSSTPLVLKATAGRLRLPEHAKALLFEVKEIRKSPFLVPGKVSIND 198
 QY 169 GSDEGLAWTVNFTGQLHGHRETGTDLGGASTQITF-----LPQFKTLBOPT 221
 DB 199 GTDEGIFSWFTVNFELGRLSKTNQ--AAALDGGSTQVTFSPPTDPOQVYDYKYNHEV- 255
 QY 222 RGYLTSEFMFNSTYKLYTHSYLGFGLKARLALATLGALETEG--TDGHTFRSACL-PRMLE 278
 DB 256 ---VTSSKKIN---VFTHSYLGLMAARHAFV---THGYKKEDTVLESVCVNPIIAN 304
 QY 279 AEWIFGGVYQYQGNQGE-----VGFEPCYAEVLVRVVGKL-----HQPVEVGSGF 326
 DB 305 RTWTYGVNVOYKVGKENGKSAEQPIVDFDAC-----LELVKRWPLVKPKPTLKQHAV 360
 QY 327 YAFSYYYDRAVDTMDIDYKGGILKVEDFERKAREVC--DNLENFTSGSPFLCWDLSYIT 384
 DB 361 AAFSYIFERATESGLVDPLAGGTTVBAVKKKAQEICAIPNDE-----QPFMCFDLTFLS 415
 QY 385 ALLKDGFGFADSTVLQTKKVNNTGMAFGATFHLQSL 423
 DB 416 TLREGFGUNDGKKIKLYKIDGHEISWALGOCAYNLTS 454
 RESULT 8
 ID Q9V018 PRELIMINARY; PRT; 464 AA.
 AC Q9V018
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)

295 KF-WNINGSSHPSCVGTTCNFVESSEIMHRELKSGSPVLPFSYFFDRALNSGLVKN 353
 346 KGGILKVDDEPKAREVC---DNLENFTSGSPFLCMLDLSVITALLKDGSGEADSVLQL 401
 354 EGGKIELOFQKAEAIACRRKTEIDDSGNWQCLDLYIYSLLDGQYFEDNQPLVL 413
 402 TKKVNNIETGVALGATF 418
 414 AKKIKGMEVSMQGLAF 430

RESULT 10
 Q8CH23
 ID Q8CH23 PRELIMINARY; PRT; 278 AA.
 AC Q8CH23;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to econucleoside triphosphate diphosphohydrolase 6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RA Strausberg R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC038126; AAH38126.1;
 KW Hydrolase.
 SQ SEQUENCE 278 AA; 30130 MW; 75A92DD1AC76297F CRC64;

Query Match 26.4%; Score 593; DB 11; Length 278;
 Best Local Similarity 58.0%; Pred. No. 4.9e-43;
 Matches 119; Conservative 31; Mismatches 49; Indels 6; Gaps 2;

49 YGIMFDAGSTGTRIHYTVFVQKMPQQLPILEGVDSVKPGLSAFVQPKQAGTAVQGLL 108
 74 YGIMFDAGSTGTRIHYVQFA-RPPGETPTLTHTETKALKPGLSAVDVEKSAQGIQELL 132
 109 EVAKUSIPRSHWKTTPVLKATAGLRLPEHKAKALLFEVKEIFRKS-PFLVPKGSVSIMD 168
 133 NVAKQHIPPVDFWKATPLVLKATAGLRLPEHKAKALLFEVKEIFRKS-PFLVPKGSVSIMN 192
 169 GSDEGILAWTVNFLTGLQHGRSTVGTLDLGASTQITFLPQFTEGTGRTGXTLSF 228
 193 GTDEGVSAWITVNFITGLSKTPGSSVGMLDLGGSGTQITFLPVEGTQLQASPGHLTAL 252
 229 EMFNSTYKLYTHSYLGFLGLKAARLA 253
 253 QMNFRTYKLYSYRW-----CSRLLA 272

RESULT 11
 Q9UT35
 ID Q9UT35 PRELIMINARY; PRT; 556 AA.
 AC Q9UT35;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative guanosine-diphosphatase (Guanosine diphosphatase).
 GN SPAC824.08 OR GDPI.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972h-;
 RA Barrall B.G.; Rajandream M.A.; Quail M.; Seegar K.; Harris D.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]

SEQUENCE FROM N.A.
 RA Sanchez R.; Franco A.; Notario V.; Gacto M.; Cansado J.;
 RT "Characterization of a guanosine diphosphatase gene from
 RT Schizosaccharomyces pombe"; EMBL/GenBank/DBJ databases.
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL121741; AAL57338.1;
 DR EMBL; AF465240; AAL69974.1;
 DR GeneDB Spombe; SPAC824.08;
 DR InterPro: IPR000407; GDA1_CD39_NTPase.
 DR Pfam: PF01150; GDA1_CD39_1_NTPase.
 DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
 SQ SEQUENCE 556 AA; 61588 MW; 1D811E3D6A6BB85 CRC64;

Query Match 23.9%; Score 538.5; DB 3; Length 556;
 Best Local Similarity 34.4%; Pred. No. 7.7e-38;
 Matches 144; Conservative 61; Mismatches 157; Indels 57; Gaps 13;

49 YGIMFDAGSTGTRIHYTVFVQKMPQQLPILEGVDSVKPGLSAFVQPKQAGTAVQGLL 108
 134 YVIMIDAGSTGSRVHVYQFNCPNPS--PKLEEFFKMLEPGLSSFAGDPGGAASLDPLL 191
 109 EVAKUSIPRSHWKTTPVLKATAGLRLPEHKAKALLFEVKEIFRKS-PFLVPKGSVSIM 167
 192 DYAMENVPEYRRCSPIAVAKATAGLRLTGESEAKAILKSVRQHLNDYPPFPIVKGVSIL 251
 168 DCSDEGILAWTVNFLTGLQHGK-QETVGTLDLGASTQITFLPQFTEGTGRTGXTLSF 223
 252 EGSMEGIYAWITINLLGLTGKATHTSTVAVMDLGGASTQILVFPFRASDGESLVGDHK 311
 224 YLTSPFMFNSTYKLYTHSYLGFLGLKAARL-----ATLGALETGTGDTGTFERSAC 272
 312 YVLDYN--GEQVELYQHSHLGLVGLKEARKLHKFVNNAAELKSELGLG-DSTSIHPC 368
 273 L-----PRLEAEWIFGKVKYQYGGNQEVSVEPFCYAEVLRVVR-----GKLNOP 318
 369 LHLNASTLHPDSKSEASEVVFVPSLAHLSLQCRGIAEKALYKDKNCVPCSFNGVHPQ 428
 319 ---EEVQSGSFAPSYVYDRAVTDMDYKGGILKVEDFERKAREVC----- 363
 429 KTEFTDTPYILSYFYDR-----MISLGMPSFTIEDMKYLSVSCGPTYHQDASFL 483
 364 -DNLENFTSGSPFLCMLDLSVITALLKDGSGEADSVLQLTKKVNNIETGVALGATFHL 421
 484 TDALKELKE-EPWCLDLNYSILSLVSGYEIPNNRQLHTAKKIDNKELGWLGLASL 541

RESULT 12
 Q8H7L6
 ID Q8H7L6 PRELIMINARY; PRT; 489 AA.
 AC Q8H7L6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative adyrase.
 GN OSJNB001410.10.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wing R.A.; Yu Y.; Soderlund C.; Kim H.-R.; Rambo T.; Saski C.;
 RA Currie J.; Collura K.;
 RT "Rice Genomic Sequence";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC126222; AAN65004.1;
 SQ SEQUENCE 489 AA; 52799 MW; 0BF6BF15448BD38E CRC64;

Query Match 23.0%; Score 518.5; DB 10; Length 489;
 Best Local Similarity 34.0%; Pred. No. 3.4e-36;
 Matches 143; Conservative 70; Mismatches 149; Indels 59; Gaps 16;

QY 46 STLYGIMFADAGSTGTRIHVTVFQKMGQPLPIL-----EGEVDSVVKPGLSAFVDQPKQGA 101
 DB 84 STRYAVTFDAGSGSRVHVYCF-----DGNLDLPIGKEIELEFKQKPKGLSAYAMPQEA 139
 QY 102 ETVOGLLEVAKDSIPRSHMKKTPVWLKATAGLRLLEKAKALLPEVKIIFR-KGPFILVP 160
 DB 140 KSLVLLLEBAEKVIPVELRQTPVRVCATAGLALGTESKSEILQAVRDLLODKSFRSQ 199
 QY 161 KGSVIMDGSDEGLAWTVNFLTQGLHQRQSTVGTLOLGGASTQITFLPQFETLEOT 220
 DB 200 PEWTVLDGSGOEAFQVNTVNYLLGNLKGPKYSHTVGVLDGGSGVQWYAIAS-EKDAGKA 258
 QY 221 P-----RGYLTSPFEMNSYKLYTHSYLGFGLKAARLATLGALETEGDTGHTFRSACLP 274
 DB 259 PPAVAGEDSVKELLKGTYYLYVHSYLYGLLAARAEILKAGE-----GNDYRN-CML 312
 QY 275 RWLEAEWIFGVKYQYGGNAGEVGFECYAEVLRVVRGKLHOPE----- 319
 DB 313 EGHGQYRYGDDIPEASGLSSG-ASYSKRAVAVRAL--KVDFPACTHMKCTFGGVWNGG 369
 QY 320 --EVQSGSFYAFSYVDRAVDMDIDYKGGILKVE--DFERKAREVCD-NLENFTS--- 371
 DB 370 GGDQCKNLFA-SFFPRAAEAGFVN-PKAPPKAVPSPDEEAAKRVCKLVKQDAQATYP 427
 QY 372 -----GSPFLMDLSYITALLKDGFGFADSTVLTQTKV-----NNIETGALGATPHLQ 422
 DB 428 DVSEENVYLCMDLVQYVTLVDGFGVDYQDITLVKVKPYSNFSFVEAAWPLGSAEYAS 487
 QY 423 S 423
 DB 488 S 488

RESULT 13
 Q8TGH6 PRELIMINARY; PRT; 599 AA.
 AC Q8TGH6;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Guanosine diphosphatase (EC 3.6.1.42).
 GN GDAL.
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hertero A.B.;
 RT "The Golgi Gpase of the fungal pathogen Candida albicans Affects morphogenesis, glycosylation and cell wall properties."
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ421721; CAD18870.1; -;
 DR InterPro; IPR000407; GDAL_CD39_NTPase.
 DR Pfam; PF01150; GDAL_CD39; 1.
 DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
 KW Hydrolyase.
 SQ SEQUENCE 599 AA; 65952 MW; D5BC3A4F6E1B646A CRC64;

Query Match 22.9%; Score 515.5; DB 3; Length 599;
 Best Local Similarity 32.6%; Pred. No. 8.5e-36;
 Matches 143; Conservative 65; Mismatches 148; Indels 83; Gaps 15;

QY 49 YGIMFDAGSTGTRIHVTVFQKMGQPLPILGEVDSVVKPGLSAFVDQPKQGAETVQGLL 108
 DB 163 YVWIDAGSTGSRVHVYCFV--KPPQLLSEFEMLKGLSFDFTDVGAAKSLDPL 220
 QY 109 EVAKDSIPRSHMKKTPVWLKATAGLRLLEKAKALLFEV-KEIFRKSPLVPGK-SVSI 166
 DB 221 EVALKKVPKQKQSTPVAVKATAGLRLIGETSKAILDEVRSHLEKDYPAVVSDEG1S1 280
 QY 167 MDGSDGGLAWTVNFLTQGLH-QHROETVGTLDLGGASTQITFLPQFETLEOTPRGVL 225

DB 281 MDGKDEGVAVWTANVYLLGNIGGKEKLPANFOLGGSGSTQIVFEPOYK--VDEVPDGE 338
 QY 226 TS--PEMENSTYKLYTHSYLGFGL-----KAARLATLGALETEGDTGHTFR----- 269
 DB 339 TKYHFTFGDQYTLYQSHLGYGLMQGRNKNVQLVKNKLSLNLQKYTKKEVKGAKATV 398
 QY 270 ---SACIPLMLEAG-----WIFGGVKYQYGG---NOEGEV 298
 DB 399 DVSNPCIPPGVAAKQVQVDELGEDEFYVVMKMGSSKDSSTVAGGSCQRYLAELVNLKDAEC 458
 QY 299 GFEPYAEVLRVVRGKLHOPEEV-----QSGSFYAFSYVDRAVDMDIDYKGGILKVED 354
 DB 459 TSKECSF-----NGVHQPSLRTFNKNSDMVFSFYDRTNPIGW-----PSSFSVEE 506
 QY 355 PERKAREVC-----DNLENFTSGSPFLMDLSYITALLKDGFGFADSTVLTQ 402
 DB 507 LKDSLKVLQCOGETFWKDIILDDHVKNLNE-EPQWCLDSLFTAMLHTGVDIPLHRELKTA 565
 QY 403 KKVNNIETGALGATPHLL 421
 DB 566 KTDNNELGCLGASLPLL 584

RESULT 14
 Q9HEM6 PRELIMINARY; PRT; 522 AA.
 AC Q9HEM6;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Guanosine diphosphatase.
 GN GDAL.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MG1/2;
 RX MEDLINE=21319012; PubMed=11425802;
 RA Lopez-Avalos M.D., Uccelletti D., Abeijon C., Hirschberg C.B.;
 RT "The UDPase activity of the Kluyveromyces lactis Golgi Gpase has a role in uridine nucleotide sugar transport into Golgi vesicles."
 RL Glycobiology 11:413-422(2001).
 DR EMBL; AJ401304; CAC21576.1; -;
 DR InterPro; IPR000407; GDAL_CD39_NTPase.
 DR Pfam; PF01150; GDAL_CD39; 1.
 DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
 SQ SEQUENCE 522 AA; 56863 MW; A7A27902607A6732 CRC64;

Query Match 22.7%; Score 511; DB 3; Length 522;
 Best Local Similarity 33.8%; Pred. No. 1.7e-35;
 Matches 147; Conservative 59; Mismatches 149; Indels 80; Gaps 17;

QY 49 YGIMFDAGSTGTRIHVTVFQKMGQPLPILGEVDSVVKPGLSAFVDQPKQGAETVQGLL 108
 DB 97 YVWIDAGSTGSRVHVYCF--DVCTQPTTLINTFEMLKGLSFDIDA/GAAKSLDPL 154
 QY 109 EVAKDSIPRSHMKKTPVWLKATAGLRLLEKAKALLFEV-KEIFRKSPLVPGK-SVSI 166
 DB 155 KIAMDVAPKORNCNCTPVAVKATAGLRLMLGDEKSSKILAQVRKHLEQDYPFPVVDGDSVI 214
 QY 167 MDGSDGGLAWTVNFLTQGL-HGHROETVGTLDLGGASTQITFLPQF--EKTLEOTPR 222
 DB 215 MDGEEGVAVWTANVYLLGNIGAGSKLPANFVLGGSGSTQIVFEPSFPPEKXNDGEHK 274
 QY 223 GYLTSPFEMNSYKLYTHSYLGFGLKAAR-----LATLGALETEGDTGHTFR--SA 271
 DB 275 -YELSPG--GHDYTLQYFSLGYGLMQGRNKNINTELWNVAISSGTTIKGTARTYELSSP 331
 QY 272 CLPRLAEW-----IFGGVKYQYGG-----NOEGEVGFEPYCVAEVL 308
 DB 332 CLPPTTAAOEKVKISDDEIYTVNFGPKVPAGPQCRYLADKILNKDKCNTPPCSF--- 388

Db 385 LTDAKRPVVCMDLLYQHVLVHGFGGLGPRKEITVGEIGIQNSVVEAAWPLGTAVEAISA 444
QY 424 L 424
Db 445 L 445
Search completed: November 13, 2003, 06:19:43
Job time : 63 secs

QY 309 RVVRGKLPQREV-----QRGSFYAFSYVDRAVDTMDIDYKGGI---LKVEDFERKARE 361
Db 389 ----NGIHQSLVHTFKETSDLVFSFYDRT-----QPLGLPSTLQELQDLART 436
QY 362 VCDNLENFTS-----GS-----PFLCWDLSYITALLKDGFGFADSTVLQTKKNNI 408
Db 437 VCNGEEVWESVFGIEGSLSELSKEPQWCLDNFQVSLHTGYDIPLORELRKTAKTIANN 496
QY 409 ETGWALGATPHLOS 423
Db 497 EUGMCLGASLPLES 511

RESULT 15

Q9SPM6 PRELIMINARY; PRT; 455 AA.
AC Q9SPM6
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Nod factor binding lectin-nucleotide phosphohydrolase.
GN LNP.
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX NCBI_TaxID=3879;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root;
EX MEDLINE=99444909; PubMed=10517321;
RA Roberts N.J., Brigham J., Wu B., Murphy J.B., Volpin H.,
RA Phillips D.A., Ezzi M.E.;
RT "A Nod factor-binding lectin is a member of a distinct class of
RT apyrases that may be unique to the legumes."
RL MGI. Gen. Genet. 262:261-267(1999).
DR EMBL; AF156782; AAF00611.1;
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; 1
DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
KW Hydrolase; Lectin.
SQ SEQUENCE 455 AA; 49879 MW; 68122846D7EC261B CRC64;

Query Match 22.6%; Score 507.5; DB 10; Length 455;
Best Local Similarity 34.0%; Pred. No. 2.7e-35;
Matches 143; Conservative 65; Mismatches 152; Indels 61; Gaps 16;

QY 47 TLYGIMPAGSTGTRIHVYTFVQKMPGOLPIL-----EGEVFDSVKPGLSAFVDPKQGA 102
Db 43 TSYAVIFDAGSTGRVHYHFDQ----NLDLLHIGNDIEFVDKIKPGLSAYGDNPEQAAK 98
QY 103 TVQGLEVAKDSIPRSHMKTPVVLKATAGLRLPEHKAKALLPEVKEIF-RKSPFLVPK 161
Db 99 SLIPLEAEADVPEDLHPKTPRLCATAGLRLNGDAAEKILQATRMFNSRSTLNVR 158
QY 162 GSVSIMDSDEGILAWVTNFLTQGLHGHROETVGTLDLGGASTQITFLPQFKTEQTP 221
Db 159 DAVSIIDTQEGSYMWVTNVTNVLNGLKSFSTKSGVIDLGGSGVQMTYAVS-KTKAKNAP 217
QY 222 R-----GYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETGDTGHTFSACLPR 275
Db 218 KVADGEDPYIKKLVKQYDLYVHSYLRFGKEATRAQVLNA--TNGS-----ANPCILP 270
QY 276 WLEAEWIFGVKQYGVNGQEGEVGFPCYAEVLRVVRGKLHQPVEVQVGRSF----- 326
Db 271 GFNGTFTTSYGVYKAFSPSSGS-NFDDCKEILKVL--KVNDPCYPSPCTFGGIWNGGG 327
QY 327 -----YAFSYVDRAVDTMDIDYK--GGILKVEDFERKAREVCD-NLENFTS----- 371
Db 328 SQCKKLFTSAFYL---AEDGVWPEPKNSILHPVDFEFAKACALNPFEDVKSTYPR 384
QY 372 ----GSPFLCMDLSYITALLKDGFGFA---DSTVLQTLTKYNN-IETGWALGATPHLOS 423

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 13, 2003, 06:13:17 ; Search time 29 seconds

(without alignments)
1419.317 Million cell updates/sec

Title: US-09-905-744B-6

Perfect score: 2250

Sequence: 1 MATSGTGFVFLVWVCVCSA.....ETGWLQATPHLLQLSLGISH 428

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	616.5	27.4	479	2 T33508	hypothetical prote
2	538.5	23.9	556	2 T33103	probable guanidine
3	489.5	21.7	455	2 S48859	nucleoside triphos
4	483.5	21.5	518	2 A40732	guanosine-diphosph
5	446.5	19.8	454	2 J4616	aprase (EC 3.6.1.
6	425.5	18.9	516	2 G84442	probable nucleosid
7	397.5	17.6	483	2 D86276	hypothetical prote
8	387.5	17.2	485	2 T34147	hypothetical prote
9	372.5	16.6	557	2 T16696	hypothetical prote
10	372.5	16.5	630	2 S50163	hypothetical prote
11	351.5	15.6	510	2 I56242	lymphoid cell acti
12	347.5	15.4	572	2 T40856	probable nucleotid
13	329.5	14.6	405	2 E86276	hypothetical prote
14	274.5	12.2	1052	2 T04439	hypothetical prote
15	248.5	11.0	508	2 C86276	7A19.33 protein -
16	138.5	6.1	628	2 A55421	nucleoside-triphos
17	110.5	4.9	497	1 J2192	subtilisin-like pr
18	106.5	4.7	553	1 G1BPVS	gene 1 protein - s
19	105.5	4.7	774	2 T45555	DNA polymerase hom
20	104.5	4.6	684	2 T47694	probable serine/th
21	104.5	4.6	4427	2 P06377	polyketide synthas
22	102.5	4.6	1019	2 T40813	probable cell divi
23	101.5	4.5	535	2 P97910	glucan 1,6-alpha-g
24	101.5	4.5	1151	2 T13347	hypothetical prote
25	99.5	4.4	535	2 C95040	glucan 1,6-alpha-g
26	99.5	4.4	548	1 HYESS	bacillolysin (EC 3
27	97.5	4.3	604	2 F89453	protein F35H12.4 (
28	97.5	4.3	654	2 AG3522	iron-regulated out
29	97	4.3	1220	2 T18291	patched protein -

30	96	4.3	711	2 S66749	hypothetical prote
31	95.5	4.2	2076	2 S15993	fatty-acyl-CoA syn
32	95	4.2	652	1 J22191	subtilisin-like pr
33	93	4.1	478	2 F90497	hypothetical prote
34	93	4.1	635	1 T37835	probable phosphoe
35	93	4.1	962	2 J55571	subtilisin-like pr
36	93	4.1	969	1 A39490	subtilisin-like pr
37	93	4.1	975	2 J55570	subtilisin-like pr
38	92	4.1	290	2 A87312	coproporphyrinogen
39	92	4.1	528	2 S13641	H+-transporting tw
40	91	4.0	417	2 H70174	glycine hydroxymet
41	91	4.0	477	2 J50597	t-plauminogen acti
42	91	4.0	500	2 D83984	gluconate kinase g
43	91	4.0	726	2 A80122	probable ferric si
44	90.5	4.0	301	2 E71482	phosphatidylserine
45	90.5	4.0	377	2 C82113	succinyl-diaminopi

ALIGNMENTS

RESULT 1

T23508
hypothetical protein K08H10.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000

C;Accession: T23508

R;Gardner, A.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19750

A;Accession: T23508

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-479 <MIL>

A;Cross-references: EMBL:283113; PIDN:CAB05544.1; GSPDB:GN00023; CESP:K08H10.4

A;Experimental source: clone K08H10

C;Genetics:

A;Gene: CESP:K08H10.4

A;Map position: 5

A;Introns: 36/3; 83/3; 189/1; 300/2; 412/3

C;Superfamily: nucleoside triphosphatase chromatin-associated

Query Match	27.4%	Score	616.5	DB 2	Length	479			
Best Local Similarity	34.3%	Pred. No.	1.3e-43						
Matches	150	Conservative	81	Mismatches	167	Indels	39	Gaps	16
QY	9	FTWLWVS--CVCASVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFAGSTGTIHYVT	66						
DB	6	FTSLILSFSLSSVVTTKTQY--WCHGDGVN---NQHTCRFFTTVIDAGSTGTRLLHYK	60						
QY	67	FVQK-----MFGQLPILEGEVPSVKPGLSARVDQPKQGAETVQGLLEVAKDSIPRSH	119						
DB	61	FIHDPATASHGMFFK--VEKEIFQEVKPLGSSFAKSSSAADSLEPLQARKEVPHFM	117						
QY	120	WKRTPVVLKATAGLRLLPEHKAKALLFEVKE--IFRKSPLVPKGSVIMDSGDEGLAW	178						
DB	118	WEKTPITLKATAGLRLLPGDMADDILESVEERIFNSGFAAPPDAVAVWPGSDGVVSWF	177						
QY	179	TUNFLTQGLH-----GHR---QETVGLDLGGASTQTFLPQFEKTLQPTGRVLTSP	229						
DB	178	TLNILETLFTDEPTVGHKPAHRSVAAPDLGGSGTQLTYPWNEAVESEHV--GYERDID	236						
QY	230	MFNSTYKLYTHSYLGFGLKAARLATLGALETG--TDGHTFRSACLPRWLE--AWIFGVG	286						
DB	237	FFGHHIRLFTHSPFLNGLIAARLNIL-QLETDNEIESTHQLITSCMPEGYQLTEWEY--AL	294						
QY	287	KYQYGNQGEVGFPCYAEVLRVVR--GKLHQPEVQVQGSFYAFSYVYDRAVDTMDIYE	345						
DB	295	KF--WNINGSSSHSFSCYGTTKNFVESSEIMHLRELKGLSPVLFYSYFDFRALNSGLV	353						
QY	346	KGGLKVEDFERKAREVC-----DNLENTSGSPFLCMDLSYITALLKDGFGFADSTVLQ	401						
DB	354	EGGKIELRQFKAABIACRREKTEIDDDGSHWMPQCLDLTYISLDGYQFEDNQPLVL	413						

QY 402 TKKVNNETGALGATF 418
 Db 414 AKKIGNEVWGQGLAP 430
 RESULT 2
 T39109
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T39109
 R:Barrell, B.G.; Rajadream, M.A.; Quail, M.; Seegar, K.; Harris, D.
 submitted to the EMBL Data Library, October 1999
 A:Reference number: Z21828
 A:Accession: T39109
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-556 <BAR>
 A:Cross-references: EMBL:AL121741; PIDN:CA857338.1; GSPDB:GN000666; SPDB:SPAC824.08
 A:Experimental source: strain 972h-; cosmid c824
 C:Genetics:
 A:Gene: SPDB:SPAC824.08
 A:Map position: 1
 Query Match 23.9%; Score 538.5; DB 2; Length 556;
 Best Local Similarity 34.4%; Pred. No. 5.7e-57;
 Matches 144; Conservative 61; Mismatches 157; Indels 57; Gaps 13;
 QY 49 YGIMFAGSTGTRIHYVTFVQKMPGQLPILEGEVDSVKPGLSAFVDPKQGAETVQGLL 108
 Db 134 YVLMIDAGSTGSRVHVYQFNCPNS--PKLEEFFKWIPEGLSSPAGDEGAASLDPLL 191
 QY 109 EVAKOSIPRSHWKTTPVLKATAGLRLPEHAKALLFVKIIFRKS--PFLVPKGSVIM 167
 Db 192 DYAMENVPBEYRRCPIAVKATAGLRLTGESEAKILKSVRQHLNDYFPFIVKDGVSIL 251
 QY 168 DGSDEGLAWVTNFTLQGLHGR--ROBTCTLDLGGASTQITFLPQFETLQTPRG--- 223
 Db 252 EGSMEGIYATITNYLLGLTGKATHTVAVMDLGGASTQVLPFRFASDGSLSVDGSHK 311
 QY 224 YLTSFEMFNSTYKLYTHSYLGLFGLKAARL-----ATLGALETEGTGHTFRAC 272
 Db 312 YVLDYN--GQVLEYQHSHLGYLKEARKLIHKFVLNNAEALKESLELIG-DSTSIHPC 368
 QY 273 L-----PRLAEWTFGGVYQYGNQGEVGFPCYAEVLVRV---GKLRQP 318
 Db 369 LHLNASTHPDSKSEAEVVFVGPDLAHLSLQCRGIAEKALYKDKNCPVPCSFNGVRQP 428
 QY 319 ---EVQVQGSFYAFSYVYDRAVDMDIDYKGGILKVEDPERKAREVC----- 363
 Db 429 KFTETFTDPSIYLISFYDR-----MISLGMPTFTIEDMKVLANSVCSGPTYWQDAFSL 483
 QY 364 -DNLNFTSGSPFLCWDLSYITALLXDGFGFADSTVLQTKKVNITGALGATFHLL 421
 Db 484 TDALKELKE-EPENCWLDNIMISLSVGEIIPNNRQHTAKIDNKELGWLGLGASLSML 541
 RESULT 3
 S48859
 nucleoside triphosphatase precursor, chromatin-associated - garden pea
 C:Species: Pisum sativum (garden pea)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Sep-1999
 C:Accession: S65147; S48859
 R:Heisch, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.
 Plant Mol. Biol. 30, 135-147, 1996
 A:Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated, chromatin
 A:Reference number: S65147; MUID:96157404; PMID:8616230
 A:Accession: S65147
 A:Molecule type: mRNA
 A:Residues: 1-455 <HS2>
 A:Cross-references: EMBL:Z32743; NID:9563611; PIDN:CAA83655.1; PID:g563612
 C:Superfamily: nucleoside triphosphatase chromatin-associated

C:Keywords: nucleus
 Query Match 21.7%; Score 489; DB 2; Length 455;
 Best Local Similarity 33.7%; Pred. No. 6e-33;
 Matches 140; Conservative 62; Mismatches 160; Indels 54; Gaps 14;
 QY 49 YGIMFAGSTGTRIHYVTFVQKMPGQLPILEGEVDSVKPGLSAFVDPKQGAETVQGL 107
 Db 44 YAVVFDAGSTGSRVHVYHFNQML-DLLHIGKGVYNNKITPGLSSYANNPEQAASLIPL 102
 QY 108 LEVAKOSIPRSHWKTTPVLKATAGLRLPEHAKALLFVKIIFRKS--PFLVPKGSVSI 166
 Db 103 LEQAEADVDPDOLQPKTPVRLGATAGLRLDNGASEKILQSVDRDMLSNRSTFNQVDAVSI 162
 QY 167 MDGSDREGILAWVTNFTLQGLHGRQETVGTLDLGASTQITFLPQFETLQTPR--- 222
 Db 163 IDGTQSGSYLWVTNVALGNLGGKYYTKTVGVVIDLGGSVQMAVAVS--KKTAKNAPKAVDG 221
 QY 223 --GYLTSFEMFNSTYKLYTHSYLGLFGLKAARLALGALTEGTGHTFRS--ACLPRMLE 278
 Db 222 DDFYIKKVLKGIPIYDLYVHSHYLFHFGREASRAELKL-----TPRSPNCLLAGFN 272
 QY 279 AEWIPGGVYQYGNQGEVGFPCYAEVLVRVGRKLPQITSGKEIEYQDAIVEAANPLGNVAEISAL 424
 Db 273 GIYTSGEPEKATAYTSG--ANFNKCKNTIRKAL--KLNYPQCPYQNCFTFGIWNQGGGNGQ 329
 QY 327 ---YAFSYVYDRAVDMDIDYKGG--ILKVEDPERKAREVC--NLENFTSGSPFL----- 376
 Db 330 KNLFASSSFYLPEDTGMVDASTPFIPLRPVDTETKAKACALNFEDAKSTYFFLDKKNV 389
 QY 377 ---CWDLSYITALLXDGFGFADSTVLQTKKVN---JETGWLGAATFHLLQSL 424
 Db 390 ASYVCMDDLIYQVLLVDGFGGLDPLQITSGKEIEYQDAIVEAANPLGNVAEISAL 445
 RESULT 4
 A40732
 guanosine-diphosphatase (EC 3.6.1.42) - Yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YEL042w
 C:Species: Saccharomyces cerevisiae
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Sep-2000
 C:Accession: A40732; S30837; S50502
 R:Abelion, C.; Yanagisawa, K.; Mandon, E.C.; Hausler, A.; Moremen, K.; Hirschberg, C.B.
 J. Cell Biol. 122, 307-323, 1993
 A:Title: Guanosine diphosphatase is required for protein and sphingolipid glycosylation
 A:Reference number: A40732; MUID:93308137; PMID:8391537
 A:Accession: A40732
 A:Molecule type: DNA
 A:Residues: 1-518 <ABE>
 A:Cross-references: EMBL:L19560; NID:g349392; PIDN:AAA34656.1; PID:g349393
 A:Note: sequence extracted from NCBI backbone (NCBIN:134708, NCBIP:134711)
 A:Accession: B40732
 A:Molecule type: protein
 A:Residues: 125-144; 238-257; 276-281; 366-374; 399-412 <AB2>
 R:Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Schl, P.; Komp, C.; Wei, Y.; Taylor,
 submitted to the EMBL Data Library, February 1993
 A:Reference number: S30812
 A:Accession: S30837
 A:Molecule type: DNA
 A:Residues: 1-518 <MUL>
 A:Cross-references: GB:U18779; EMBL:L10830; NID:g503625; PIDN:AB65000.1; PID:g603637
 R:Dietrich, F.S.
 submitted to the EMBL Data Library, December 1994
 A:Description: The sequence of S. cerevisiae cosmid 8199, 8334, and 9871.
 A:Reference number: S50491
 A:Accession: S50502
 A:Molecule type: DNA
 A:Residues: 1-518 <DIE>
 A:Cross-references: EMBL:U18779; NID:g603625; PIDN:AB65000.1; PID:g603637; MIPS:YEL04;
 C:Genetics:
 A:Gene: SGD:GDAL
 A:Cross-references: SGD:S0000768; MIPS:YEL042w
 A:Map position: 5U

```
A:Residues: 1-516 <STO>
A:Cross-references: GB:AE002093; NID:g3461821; PIDN:AAC32915.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g02970
A:Map position: 2
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match      18.9%; Score 425.5; DB 2; Length 516;
Best Local Similarity 30.6%; Pred. No. 1.5e-27;
Matches 127; Conservative 61; Mismatches 154; Indels 73; Gaps 13;

QV    42 NVASATLYIGMFAGSGTGTRIHVVTYFQKMGQLPILE--GEVFDSVK--PGLSAPVDQP 97
      |||||
      |||||
```

A;Cross-references: GB:U58597; NID:gl381632; PID:gl381633
A;Accession: PC4147
A;Molecule type: protein
A;Residues: 59-95;96-131;132-160;236-253;332-345 <HA2>
A;Experimental source: tubers
A;Note: The authors translated the codon GCA for residue 215 as Gly
C;Comment: This enzyme belongs to a family of E-type ATPases, and it catalyzes the hydrolysis of nucleoside triphosphates. The enzyme has nucleotide substrate specificity, divalent cation requirement, and insensitivity to vanadate.
C;Genetics:
A;Gene: rropl
C;Superfamily: nucleoside triphosphatase chromatin-associated
C;Keywords: Glycoprotein; hydrolase; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;8-25/Domain: transmembrane #status predicted <TM>

Db 61 NLRGSLRVSVVDDGSGTGTRHVFY--RIESGKVPFPRGANYASIKLHPGLSAPADDP 118
 QY 98 KQGETVQGLLEVAKDSIPRSHWKTTPVLKATAGLRLPEHAKALLFEVKEIFRKSPP 157
 Db 119 DGASVSLTELVEFAKGVPRKGMJTIETVRLMATAGMRLLELPVQEKILGVARRVLKSSGF 178
 QY 158 LVPKGSVIMDSDEGLIAWTVNFLTQGLHGRQETVGTDLGGASTQITFL-----P 211
 Db 179 LPRDEMASVIGSDGAVVAVANFALGSLGDPKTKTIGIVELGGASQVTFVSSSPMP 238
 QY 212 QFEXTLEOTPRGYLTSEMFMNSTYKLYTHSVLGRGLKAARLATLGA-----ETEGTD 264
 Db 239 EFSRTI-----SFG--NVTYLYSHSFLHPGQNAHDKWGLSLLSROHNSAVEPTR 287
 QY 265 GHTRSAACLP-----WLEAEWIFGKVKYQGNQGEVGEVGFPCVAELRVV 311
 Db 288 EKIFDPCAPKYNLDANTQKLSGLAEBESRLSDSFQAGN-----YSQCRSAALTIL 341
 QY 312 RGKUHQPVEVORGSGFYAFSYYYDRAVDTMI-----DYKGGILKVEDPERKAREV 362
 Db 342 QDNGRILIIITAGSFLFPGGKAWLSNMISAGERFCGEDWAK---LRVKDPSLHEBDL 398
 QY 363 CDNLENFTSGSPFLCMDSYITALLKDGQGF-ADSTVLQLTKKVNIETGMALGA 416
 Db 399 LR-----YCFSSAYIVSLHDTLGIPLDDEIRIGYANQAGDIPLOWALGA 442

RESULT 7
 D86276
 Hypothetical protein F7A19.34 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 18-Nov-2002
 C:Accession: D86276
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizuar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, G.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 C:Accession: D86276
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-483 <STO>
 A:Cross-references: GB:AE005172; NID:G5080801; PIDN:AAD39311.1; GSPDB:GN00141
 C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 17.6%; Score 397; DB 2; Length 483;
 Best Local Similarity 27.6%; Pred. No. 3.3e-25;
 Matches 120; Conservative 71; Mismatches 162; Indels 82; Gaps 17;

QY 32 GFLSMCPINVASLTIGIMFDAGSTGTRHVV--YFVQKMPQLPILGEVFD----- 84
 Db 59 GLLSRCKLR-----YSVLIDAGSGSTRVHVFGYNFESGKP-----VFDFGEKH 103
 QY 85 ----SVKGLSFAVDPQKGAETVQGLEVAKDSIPRSHWKTTPVLKATAGLRLPEH 140
 Db 104 YANLKITFGLSSYADNPEGASVSVTLVFEFAKQRIKPMFRPSDIRLWATAGMELLEVPV 163
 QY 141 AKALFEVKEIFRKSFPFLVPKGSVIMDSDEGLIAWTVNFLTQGLHGRQETVGTGLD 200
 Db 164 QEQILEVTRVRLRSSGFMFRDEWANNVISGSDGIYSWITANYALGSLGTDPLETTGIVEL 223
 QY 201 GASTQITLPPQFEXTLEOTPRGYLTSEMFMNSTYKLYTHSVLGRGLKAARLATLGALET 260
 Db 224 GSAQAQVTV-----SSEHVPEYSETIAYGNISYIYSHSFLDYGKDAALKLLEKLN 278

QY 261 EG---TDGHTFRSACLPRLWEAWIF--GGVKYQYG-----GNQGEVGFPCYAE 306
 Db 279 SANSTVDG--VVEOPCTPK---GYVDTSKNYSSGFLADESKLQSGLOAGNFSKCRSA 333
 QY 307 VLRVVR-----CKLHQPVEVORGSGFYAFSYYYDRAVDTMIDYKGGILKV- 352
 Db 334 TFALLKREGKENCIVHSCISGTTTPO--LQGSFLATASFYITAKFFEL--EEKGMUSELI 389
 QY 353 -----EDPERKAREVCDNLENFTSGSPFLCMDSYITALLKDGQGF--DSTVLQUT 402
 Db 390 PAGKRYCGEWSKLLILSYPTTDEYLGR-----YCFSAAYITISMLHDSLGIALDDESITYAS 446
 QY 403 KK--VNNIETGMALGA 416
 Db 447 KAGEKHIPLDOWALGA 461

RESULT 8
 T34147
 Hypothetical protein C33H5.14 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Mar-2000
 C:Accession: T34147
 R:Bradshaw, H.; Stelliyes, L.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid C33H5.
 A:Reference number: 221482
 A:Accession: T34147
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-485 <BRA>
 A:Cross-references: EMBL:U41007; PIDN:AAA82272.1; CESP:C33H5.14
 A:Experimental source: strain Bristol N2
 C:Genetics:
 C:Gene: CESP:C33H5.14
 A:Introns: 22/1; 83/1; 120/2; 167/1; 269/3; 399/3
 C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 17.2%; Score 387.5; DB 2; Length 485;
 Best Local Similarity 27.7%; Pred. No. 2.1e-24;
 Matches 120; Conservative 84; Mismatches 152; Indels 77; Gaps 18;

QY 49 YGIMFDAGSTGTRHVVTFVQKMPQLPILGEVFD-----VKPGLSFAVDPQKGA 102
 Db 25 YGVICDAGSGSTRFLFVVT-LKPLSGGLTNITDLIHESEPVVKKVTPGLSGDKPEQVVE 83
 QY 103 TVQGLEVAKDSIPRSHWKTTPVLKATAGLRLPEHAKALLFEVKEIFRKSFPFL-VPK 161
 Db 84 VLTPLLRFAEHIPEYQELGETDILLIFATAGMRLPEKQDAILNQLNGLSVTLRVSD 143
 QY 162 GSVSIMDSDEGLIAWTVNFLTQGLHGRQETVGTGLDGAQTITFLPQEPK----- 215
 Db 144 SNIRIIDGAWEGIYSWITAVNVLGRFDKENDSKVGMIDMGASVQIAFAFANESYNGG 203
 QY 216 TLEQTPRYLTSEFMENSTYKLYTHSVLGRGLKAARLATLGALETGDTGHTFRSACLP 275
 Db 204 NYEINLGSISTNEDYK--YKIYSTFLGYGANEGLKYYENSLVKSNS-----NDSCSP 257
 QY 276 WLEASWIFGKVKYQGNQGEVGEVGFPCVAELRVVGRGLHQPE----- 319
 Db 258 GLNR--LTG-----EFTVNGTGE--WDVLAQVSSLI--GDKAQPSCPNPTCFLRNVIAPSV 308
 QY 320 EVQRGSFYAFS--VYDRAVDTMIDYKGGILKVEDPERKAREVC---DNLENFTSGSP 374
 Db 309 NLSTVOLIGFSEYWTTS-----NFGSGEYHYQKFTDEVKVCQKQWINDIQGFKRNE 362
 QY 375 F-----LCMDLSYITALLKDGQGFADST--VLQLTKVNNIETGMALGA----- 416
 Db 363 FENADIERLGTNCFAAWTVSLHDGFN--VDKTKHLFQSVLKIAGEMQWALGAMLYHSH 421
 QY 417 --TFHLLQSLGIS 427
 Db 422 DLKFNLEQLLEVA 434

Db 152 VERSLSNYPF--DFQARIITGOEGAYGWITINYLKGFQSKTRWFSVVPYETNNQETTF 209
 QY 196 GTLDLGGASTQITLPPFEXTLEOTPRGYLTSFEMFNSTYKLYTHSYLVGFLGKARLAL 255
 Db 210 GALLDGGASTQITFVPO--NOTIE-SPDNAL-QPRLYGKDNVYTHSFCLCYGKQDALWQKL 266
 QY 256 GALTETGDTGHTFRSACL-----PRMLEAEWIFGGVKYQYGGNQORGE 297
 Db 267 -AKDIQVNASNEILRDPCHFGYKVVNVSDLYKTPCTKRFEMTLPPFQPEIQIQIGN---- 321
 QY 298 VGPEPCYAEVLRV-----VRGKLHQPEEVQSGSFYAFSYVYVYDRAVDTDMDIVE 345
 Db 322 --YQCHQSILELENTSYCPYSQCAFNGIFLPLQDGFAPAF-IVWKFLN---UTSE 375
 QY 346 KGGILKVEDPERK-AREVCNLENFTSG--SPFL---CMDLSYITALLKDGFGF-ADS-T 397
 Db 376 KVSQEKVETMMKKECAQPMEEIKTSYAGVKEKYLSEYCPSTGVSILSLQGLVYHFTADSWE 435
 QY 398 VLQUTKKVNNIETGALGATEHL 420
 Db 436 HIHFGIKTQSGDAGWTGLGYMLNL 458

RESULT 12
 T40856
 Probable nucleotide phosphatase - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T40856
 R:Ransperger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, October 1999
 A:Reference number: 221952
 A:Accession: T40856
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-572 <RAM>
 A:Cross-references: EMBL:AL121783; PIDN: CAB57847.1; GSPDB: GNM00068; SPDS: SPCC11E10.05C
 A:Experimental source: strain 972h-; cosmid c11E10
 C:Genetics:
 A:Gene: SPDB: SPCC11E10.05C
 A:Map position: 3

Query Match 15.4%; Score 347; DB 2; Length 572;
 Best Local Similarity 25.5%; Pred. No. 6.6e-21;
 Matches 115; Conservative 67; Mismatches 157; Indels 112; Gaps 16;

QY 49 YGIMFDAGSTGTRIHYVTF-----VQKMPGQLPILGEVFD-----SVKPGLSAFVD 95
 Db 5 YGIFDAGSSRLIIWSWDYDTSLSLSDKVKKLPLETIGIGDGKWSLKVQPGISSFAN 64

QY 96 QPKQ-GASTVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLL-PEHKAKALLFEVKEIFR 153
 Db 65 NPKHVGKHLKELDLFAAHAIPOKHVETPVFLSATAGMRLGLGVDAQNKLTHACRYIKK 124

QY 154 KSPFLVP--KGSVIMDSGEGILAWTVNFLTQGLHGRQETVGTLDLGASTQITFLP 211
 Db 125 NYDEDIPCMSIRIVDKAEGMGLATNLYLTKLEKOTSTVGLFDMGASVQAF-- 182

QY 212 QPEKTEPTPRGYLTSFEMFNST-----YKLYTHSYLVGFLGKARLALIGAL- 258
 Db 183 -----ELPPSLKNYKDSISTVHIGLQNGQQLVEPLFVTTWLGFGANEAYRRYLGLLI 235

QY 259 ETE-CTDGHTRFSAQLPRWLEAEWIFGGVKYQYGG-----NQGEVGFPEPCY 304
 Db 236 ESENGKVGNTLSDPCSLSR--GRTYDIDGIEFAGTGLKQCLKLTYNLLNKKDKPCSMDCPN 293

QY 305 AEVLVVRGKLHQPEEVQSGSFYAFSYVYVYDRAVDTDMDIVEKGGILKVEDFERKAREVC- 363
 Db 294 EDGISI-----PPVDPRANTEFVGVSFEPWYTTNDV-----EDMGSYHFFPFYKVDYCG 343

QY 364 -----DNLENFTSGPFLCMDLSYITALLKDGFGFADSTV----- 398
 Db 344 TEWETMLSRLYNKELTPSTDENKLEK-----LCFKASWALNVLHVEGFDVPPKNTSSND 396

QY 399 -----LQUTKKVNNIETGALG 415
 Db 397 AKDGLSVIPAVHSPFTSLEKIERTEVSWTLG 427

RESULT 13

E86276

hypoetical protein F14L17.1 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C:Accession: E86276

R:Thellogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E86276

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-405 <STO>

A:Cross-references: GB:AE005172; MID:97626666; PIDN:AAF43924.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 14.6%; Score 329.5; DB 2; Length 405;

Best Local Similarity 26.3%; Pred. No. 1.2e-19;

Matches 110; Conservative 63; Mismatches 158; Indels 87; Gaps 15;

RESULT 14

T04439

hypoetical protein T1816.150 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999

C:Accession: T04439

R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoerge, W.; Bancroft, I.; Mewes, H

submitted to the protein Sequence Database, April 1998

A:Reference number: 215359

A:Accession: T04439

A:Molecule type: DNA

A:Residues: 1-1052 <BEV>

A:Cross-references: EMBL:AL021687

A:Experimental source: cultivar Columbia; BAC clone T18B16

C:Genetics:

A:Map position: 4

A:Introns: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3

A>Note: T18B16.150

Query Match 12.2%; Score 274; DB 2; Length 1052;
Best Local Similarity 24.9%; Pred. No. 2.1e-14;
Matches 107; Conservative 70; Mismatches 171; Indels 82; Gaps 19;

QY 51 IMPDAGSTGTRIHVY--TFVQKMPGQLPIL-----EVEFD--SVKPGLSAFV 94
DB 525 LVIVISITGRAYVYQASINVKDSSDFVKNLSITGSRKSGRAYDRMETEPGDKLV 584
QY 95 DQPKQGAET--VOGLLEVAKDSIPRSHWKTTPVVKATAGLRLLPEHKAKALLFEVKEIFR 153
DB 585 NN-RTGLKTAIKPLQIAEKQIPKNAHRTTSLFVYATAGVRLRPADSSWILGNVWSILA 643
QY 154 KSPILVPKGSVIMDSDEGILAWTVNFLTGLGHG-HROETVGTDLGASTQITFLPQ 212
DB 644 KSPFTRERWIIISGTEEAYFGWTAIYOTISLGLAPKATGALDGLGSSLQVTFENE 703
QY 213 FEKTEQTPRGYLTSEFMNFTYKLYTHSYLGFGLKAA-----RLATL----- 255
DB 704 -ERTHNETN---LNLKRGSVNHLISAYSAGYGLNDAFDRSVVHLKKLNNVKNKSDLIE 758
QY 256 GALETEGTGHTFRSACLPRLAEWTFGGVQYQGNQGEVGFPE-----PCVAEVR 309
DB 759 GKLE-----MKHPCNGSYNGYQYCOCASSVQGGKKGSGVSIKLVGAPNNGECSA 810
QY 310 VVR--GKLGQBEVQR--GSFVAFSYYYDRAVDTMDIDYEGGI--LKVEDFERKAREVC 363
DB 811 LAKVAPCALPGYRPHGQFVAVSGFP-----VYREFNLSAEALDDVLEKGRFC 862
QY 364 DN-----LENFTSGSPFL---CMDSLYITALLKDGFGPADSTV-----LQLTCKVNNIET 410
DB 863 DKWQVARTSVSPQFFIEQYCFRAPHYIVSLREGLYITDKQIIIGSGSITWTGLVALLES 922
QY 411 GWALGATFHL 420
DB 923 GKALSSTLGL 932

RESULT 15

C86276

7A19.33 protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 18-Nov-2002

C:Accession: C86276

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: C86276

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-508 <STO>

A:Cross-references: GB:AB005172; NID:95080800; PIDN:AAD39310.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 11.0%; Score 248; DB 2; Length 508;
Best Local Similarity 23.3%; Pred. No. 1.1e-12;
Matches 110; Conservative 77; Mismatches 159; Indels 126; Gaps 21;

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DB 78 RVHVEGY--RIESKPVDFGEENYASLKLSPGLSAYADNPEGVSESVTELVEFAKRVH 135
QY 117 RSHWKTTPVVKATAGLRLLPEHKAKALLFEVKEIFRKSPLVPKGSVIMDSDE--GI 174
DB 136 KGKLLKSDIRLMATAGNRLLLELPVQEQILDVTRVLRSSGF-----DPRDEWASV 185
QY 175 LAWTVNFLTGLGHGROETVGTDLG-----GASTQITFLPQFKEITLQTPRGYLTSE 228
DB 186 ISEILENF-----QDLMKVYMLGLLIMRSVRLVTFV-----STELVSEFSRTL 231
QY 229 EMENSTYKLYTHSYLGFGLKAARLATLGALE---ETEGTGHGHTFRSACLPRLAEWI--- 282
DB 232 AYGNVSNLXSHSFLDFGQDAQAQEKLSLYNSAANSTGEGIVDPDPCIPKGYILETNLQK 291
QY 283 -----PGGVKQYQGNQGEVGFPEPCVAEVLVRVVR-----GKLGQBEVQGRS 325
DB 292 DLPGFLADKQKFTATLQAAGNFSECRSAFAMLQEEKGKCTYKRCSIGSIFTFN--LOGS 349
QY 326 FYAFSYVY-----DRAVDTMDI-----DVEKGGILKVEDFERKAREVCNLE 367
DB 350 FLATENFHTSKFFGLQEKELSEMILAGKRFGEESK---LKVYPTFKD-----ENLL 402
QY 368 NFTSGSPFLCMDSLYITALLKDGFGFA-DSTVLQLTKKV--NNIETGWALGA 416
DB 403 RY-----CFSSAYIISMLHDSLGVALDDEIRIKYASKAGEEDIPLDWALGA 447

Search completed: November 13, 2003, 06:20:21

Job time : 34 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

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Run on:      November 13, 2003, 06:19:46 ; Search time 44 Seconds
              (without alignments)
              1775.806 Million cell updates/sec
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Title: US-09-905-744B-6
 perfect score: 2250
 sequence: 1 MATSWGTVFFMLVSCVCSA.....ETGNALGATFHLQLSLGISH 428

Scoring table: BLOSUM62
Gapop 10.0 . Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications_AA.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	2250	100.0	428	12	US-10-286-926-3	Sequence 3, Appli	
2	2250	100.0	428	12	US-10-286-926-5	Sequence 5, Appli	
3	2250	100.0	428	14	US-10-091-085-3	Sequence 3, Appli	
4	2250	100.0	428	14	US-10-091-085-5	Sequence 5, Appli	
5	2250	100.0	428	14	US-10-092-063-3	Sequence 3, Appli	
6	2250	100.0	428	14	US-10-092-063-5	Sequence 5, Appli	
7	2235	99.3	428	12	US-10-286-926-7	Sequence 7, Appli	
8	2235	99.3	428	14	US-10-091-085-7	Sequence 7, Appli	
9	2235	99.3	428	14	US-10-092-063-7	Sequence 7, Appli	
10	2104	99.5	405	12	US-10-286-926-25	Sequence 25, Appl	
11	2104	99.5	405	14	US-10-092-063-25	Sequence 25, Appl	
12	1837.5	78.1	465	9	US-10-092-063-39	Sequence 39, Appl	
13	1660	73.8	330	9	US-09-925-299-876	Sequence 876, App	
14	1660	73.8	330	11	US-09-925-299-876	Sequence 876, App	
15	999	44.4	484	12	US-10-286-926-27	Sequence 27, Appli	

ALIGNMENTS

RESULT 1

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US-10-286-926-3
; Sequence 3, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Young, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 05/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-926-3

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Query Match 100.0%; Score 2250; DB 12; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.5e-215;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSGTFFMLVSCVCSAVSHRNQQTWFEGLSAPVDQPKGAETVQGLLEVAKDSIPRSHW 120
DB 1 MATSGTFFMLVSCVCSAVSHRNQQTWFEGLSAPVDQPKGAETVQGLLEVAKDSIPRSHW 120
QY 61 RIHVTVFQKMPGQPLILEGEVDSVKPGLSAFVDQPKGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVTVFQKMPGQPLILEGEVDSVKPGLSAFVDQPKGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTVPVLKATAGLRLPEHKAALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180
DB 121 KKTVPVLKATAGLRLPEHKAALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180
QY 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQPEKTLQTPRGYLTSEFMNSTYKLYTH 240
DB 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQPEKTLQTPRGYLTSEFMNSTYKLYTH 240
QY 241 SYLGFGLKAARLATLGALETGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
DB 241 SYLGFGLKAARLATLGALETGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
QY 301 EPCVAELVVRGKLHQPEEVQVGSFYAFSYIYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCVAELVVRGKLHQPEEVQVGSFYAFSYIYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQTLTKVNNIETGVALGATFHL 420
DB 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQTLTKVNNIETGVALGATFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 2
US-10-286-926-5
; Sequence 5, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428

TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-926-5

Query Match 100.0%; Score 2250; DB 12; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.5e-215;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSGTFFMLVSCVCSAVSHRNQQTWFEGLSAPVDQPKGAETVQGLLEVAKDSIPRSHW 120
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QY 61 RIHVTVFQKMPGQPLILEGEVDSVKPGLSAFVDQPKGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVTVFQKMPGQPLILEGEVDSVKPGLSAFVDQPKGAETVQGLLEVAKDSIPRSHW 120
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DB 241 SYLGFGLKAARLATLGALETGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
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QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 3
US-10-091-085-3
; Sequence 3, Application US/10091085
; Publication No. US20020146772A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/10/091,085
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-091-085-3

Query Match 100.0%; Score 2250; DB 14; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.5e-215;

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361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTLTKKVNNIETGALGATPHL 420
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RESULT 6

US-10-092-063-5
; Sequence 5, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-063-5

Query Match 100.0%; Score 2250; DB 14; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.5e-215;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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421 LQSLGISH 428
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RESULT 7

US-10-286-926-7
; Sequence 7, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-926-7

Query Match 99.1%; Score 2235; DB 12; Length 428;
Best Local Similarity 99.3%; Pred. No. 4.8e-214;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 61 RIHYVTFVQKMPGQLPILEGVEFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHYVTFVQKMPGQLPILEGVEFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

QY 121 KKTPTVVKATAGLRLLEPEHAKALLFEVKEIFRKSFFLVPKGSVSMDSGDEGILAWTV 180
 DB 121 KKTPTVVKATAGLRLLEPEHAKALLFEVKEIFRKSFFLVPKGSVSMDSGDEGILAWTV 180
 QY 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEXTLEQTPRGYLTSPFENSTYKLYTH 240
 DB 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEXTLEQTPRGYLTSPFENSTYKLYTH 240
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 DB 241 SYLGFGGLKAARLATLGALETEGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQGEGVGF 300
 QY 301 EPCVAEVLVRVVRGKLHQPBEVQSGSYAFSYIYDRAVDTMDIDYKGGILKVEDFERKAR 360
 DB 301 EPCVAEVLVRVVRGKLHQPBEVQSGSYAFSYIYDRAVDTMDIDYKGGILKVEDFERKAR 360
 QY 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKNNIETGMAIGATPHL 420
 DB 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKNNIETGMAIGATPHL 420
 QY 421 LQSLGISH 428
 DB 421 LQSLGISH 428

RESULT 8

US-10-091-085-7
 ; Sequence 7, Application US/10091085
 ; Publication No. US20020146772A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
 ; FILE OF INVENTION: POLYPEPTIDES
 ; CURRENT APPLICATION NUMBER: US/10/091,085
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-16
 ; PRIOR APPLICATION NUMBER: 09/122,449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/244,444
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-091-085-7

Query Match 99.3%; Score 2235; DB 14; Length 428;
 Best Local Similarity 99.3%; Pred. No. 4.8e-214;
 Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MATSGTGVFFMLVSVCSAVSHRNQQTWPEGIFLSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSGTGVFFMLVSVCSAVSHRNQQTWPEGIFLSMCPINVSASTLYGIMFDAGSTGT 60
 QY 61 RIHVTVFQKMPGQLPILGEVEFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHVTVFQKMPGQLPILGEVEFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 QY 121 KKTPTVVKATAGLRLLEPEHAKALLFEVKEIFRKSFFLVPKGSVSMDSGDEGILAWTV 180
 DB 121 KKTPTVVKATAGLRLLEPEHAKALLFEVKEIFRKSFFLVPKGSVSMDSGDEGILAWTV 180
 QY 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEXTLEQTPRGYLTSPFENSTYKLYTH 240
 DB 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEXTLEQTPRGYLTSPFENSTYKLYTH 240

DB 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEXTLEQTPRGYLTSPFENSTYKLYTH 240
 QY 241 SYLGFGGLKAARLATLGALETEGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQGEGVGF 300
 DB 241 SYLGFGGLKAARLATLGALETEGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQGEGVGF 300
 QY 301 EPCVAEVLVRVVRGKLHQPBEVQSGSYAFSYIYDRAVDTMDIDYKGGILKVEDFERKAR 360
 DB 301 EPCVAEVLVRVVRGKLHQPBEVQSGSYAFSYIYDRAVDTMDIDYKGGILKVEDFERKAR 360
 QY 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKNNIETGMAIGATPHL 420
 DB 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKNNIETGMAIGATPHL 420
 QY 421 LQSLGISH 428
 DB 421 LQSLGISH 428

RESULT 9

US-10-092-063-7
 ; Sequence 7, Application US/10092063
 ; Publication No. US20020173005A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mulero, Julio
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
 ; FILE OF INVENTION: 28110/35908
 ; CURRENT APPLICATION NUMBER: US/10/092,063
 ; CURRENT FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: 09/370,265
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: PCT/US99/16180
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 09/244,444
 ; PRIOR FILING DATE: 1999-02-04
 ; PRIOR APPLICATION NUMBER: 09/122,449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-16
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-092-063-7

Query Match 99.3%; Score 2235; DB 14; Length 428;
 Best Local Similarity 99.3%; Pred. No. 4.8e-214;
 Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MATSGTGVFFMLVSVCSAVSHRNQQTWPEGIFLSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSGTGVFFMLVSVCSAVSHRNQQTWPEGIFLSMCPINVSASTLYGIMFDAGSTGT 60
 QY 61 RIHVTVFQKMPGQLPILGEVEFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHVTVFQKMPGQLPILGEVEFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 QY 121 KKTPTVVKATAGLRLLEPEHAKALLFEVKEIFRKSFFLVPKGSVSMDSGDEGILAWTV 180
 DB 121 KKTPTVVKATAGLRLLEPEHAKALLFEVKEIFRKSFFLVPKGSVSMDSGDEGILAWTV 180
 QY 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEXTLEQTPRGYLTSPFENSTYKLYTH 240
 DB 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEXTLEQTPRGYLTSPFENSTYKLYTH 240

QY 241 SYLGFGKAAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVGF 300
DB 241 SYLGFGKAAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVGF 300
QY 301 EPCYAEVLVRVVRGKLHOPEEVRQGSFYAFSYVYDRAVDTDMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVVRGKLHOPEEVRQGSFYAFSYVYDRAVDTDMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQTKKNNIETGALGATFHL 420
DB 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQTKKNNIETGALGATFHL 420
QY 421 LOSLGISH 428
DB 421 LOSLGISH 428

RESULT 10

US-10-286-926-25
; Sequence 25, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-926-25

Query Match 93.5%; Score 2104; DB 12; Length 405;
Best Local Similarity 100.0%; Pred. No. 5.1e-201;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATSNGTVFFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSNGTVFFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTVFQKMPGOLPILGEVDFSVKGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTVFQKMPGOLPILGEVDFSVKGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTVPVLKATAGLRLLPEHKAKALLFEVKEIFRKSPLFVPGKSVSIMDGSDEGILAWTV 180
DB 121 KKTVPVLKATAGLRLLPEHKAKALLFEVKEIFRKSPLFVPGKSVSIMDGSDEGILAWTV 180
QY 181 NFLTQGLHGHROETVGTDLGGASTQITPLPQFEKLTLEQTPRGYLTSEFMFNSTYKLYTH 240

DB 181 NFLTQGLHGHROETVGTDLGGASTQITPLPQFEKLTLEQTPRGYLTSEFMFNSTYKLYTH 240
QY 241 SYLGFGKAAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVGF 300
DB 241 SYLGFGKAAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVGF 300
QY 301 EPCYAEVLVRVVRGKLHOPEEVRQGSFYAFSYVYDRAVDTDMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVVRGKLHOPEEVRQGSFYAFSYVYDRAVDTDMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQ 400
DB 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQ 400

RESULT 11

US-10-092-063-25
; Sequence 25, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-063-25

Query Match 93.5%; Score 2104; DB 14; Length 405;
Best Local Similarity 100.0%; Pred. No. 5.1e-201;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATSNGTVFFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSNGTVFFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTVFQKMPGOLPILGEVDFSVKGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTVFQKMPGOLPILGEVDFSVKGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTVPVLKATAGLRLLPEHKAKALLFEVKEIFRKSPLFVPGKSVSIMDGSDEGILAWTV 180
DB 121 KKTVPVLKATAGLRLLPEHKAKALLFEVKEIFRKSPLFVPGKSVSIMDGSDEGILAWTV 180
QY 181 NFLTQGLHGHROETVGTDLGGASTQITPLPQFEKLTLEQTPRGYLTSEFMFNSTYKLYTH 240
DB 181 NFLTQGLHGHROETVGTDLGGASTQITPLPQFEKLTLEQTPRGYLTSEFMFNSTYKLYTH 240
QY 241 SYLGFGKAAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVGF 300
DB 241 SYLGFGKAAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVGF 300

QY 301 EPCYAEVLVVRGKQLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVVRGKQLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNDLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQ 400
DB 361 EVCNDLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQ 400

RESULT 12

US-10-092-063-39
; Sequence 39, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-092-063-39

Query Match 81.7%; Score 1837.5; DB 14; Length 465;
Best Local Similarity 84.0%; Pred. No. 2.4e-174; Indels 3; Gaps 3;
Matches 353; Conservative 25; Mismatches 39;

QY 1 MATSWGTVPFMLVSVSCVSAVSHRNQQTWFEQIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGAV-FMLIIACVGVSTVYREQQTWFEQIFLSSMCPINVSAGTFYGIMFDAGSTGT 59
QY 61 RIHVYTFVOKMBGQPLILEGEVDSVKBSLSAFVDPOKQGAETVQGLLELVAKDSIPRSHW 120
DB 60 RIHVYTFVOKMBGQPLILEGEVDSVKBSLSAFVDPOKQGAETVQGLLELVAKDSIPRSHW 119
QY 121 KKTVPVVKATAGLRLLPEHAKALLFEVKEIFRKSPLVPRKGSVIMDGSDEGILAVTV 180
DB 120 ERTVPVVKATAGLRLLPEHAKALLFEVKEIFRKSPLVPRKGSVIMDGSDEGILAVTV 179
QY 181 NETGQLHGRHRETQVTDLGGASTQITFLQPEKTLBOTPRGYLTSEFENSTYKLYTH 240
DB 180 NETGQLHGRHRETQVTDLGGASTQITFLQPEKTLBOTPRGYLTSEFENSTYKLYTH 239
QY 241 SYLGFGLKAAARLATLGALETEGTDGHTFRSACLPRWLEAEWIFGVKYQYCGNQGEGVGF 300
DB 240 SYLGFGLKAAARLATLGALETEGTDGHTFRSACLPRWLEAEWIFGVKYQYCGNQGEGVGF 299
QY 301 EPCYAEVLVVRGKQLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 300 EPCYAEVLVVRGKQLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 359
QY 361 EVCNDLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKVNNIETGWLGAATFHL 420
DB 360 EVCNDLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKVNNIETGWLGAATFHL 417

RESULT 13

US-09-925-299-876
; Sequence 876, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 876
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (106)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (124)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (138)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (178)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (194)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-876

Query Match 73.8%; Score 1660; DB 9; Length 330;
Best Local Similarity 97.3%; Pred. No. 7.2e-157;
Matches 319; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 101 AETVQGLLELVAKDSIPRSHHKKTPVVLKATAGLLEHAKALLFEVKEIFRKSPLVLP 150
DB 3 ARAVQGLLELVAKDSIPRSHHKKTPVVLKATAGLLEHAKALLFEVKEIFRKSPLVLP 62
QY 161 KGSVSIIMDGSDEGILAVTVNFLTQGLHGRHRETQVTDLGGASTQITFLQPEKTLQOT 220
DB 63 KGSVSIIMDGSDEGILAVTVNFLTQGLHGRHRETQVTDLGGASTQITFLQPEKTLQOT 122
QY 221 PRGULTSEMNSTYKLYTHSYLQFGLKAAARLATLGALETEGTDGHTFRSACLPRWLEAE 280
DB 123 PRGULTSEMNSTYKLYTHSYLQFGLKAAARLATLGALETEGTDGHTFRSACLPRWLEAE 192
QY 281 WIFGVKYQYCGNQGEGVGFPCYAEVLVVRGKQLHQPVEVQSGSFYAFSYYYDRAVDT 340
DB 193 WIFGVKYQYCGNQGEGVGFPCYAEVLVVRGKQLHQPVEVQSGSFYAFSYYYDRAVDT 242
QY 341 MIDVEKGGILKVEDFERKAREVCNDLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQ 400
DB 243 MIDVEKGGILKVEDFERKAREVCNDLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQ 302
QY 401 LTKKVNNIETGWLGAATFHLQSLGISH 428
DB 303 LTKKVNNIETGWLGAATFHLQSLGISH 330

RESULT 14

US-09-925-299-876
 ; Sequence 876, Application US/09925299
 ; Publication No. US20030040617A9
 ; GENERAL INFORMATION:

APPLICANT: Rosen et al.

APPLICANT: Mulero, John

APPLICANT: Ford, John

APPLICANT: Yung, George

APPLICANT: Mulero, Julio

FILE REFERENCE: PA102

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA102

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 876

LENGTH: 330

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (97)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (106)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (124)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (138)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (174)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (178)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (194)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-299-876

Query Match 73.8%; Score 1660; DB 11; Length 330;

Best Local Similarity 97.3%; Pred. No. 7.2e-157;

Matches 319; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 101 AETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSPLVLP 160

DB 3 ARVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSPLVLP 62

QY 161 KGSVSIMDSDEGILAWVTNFTVGLGHRQETVGTLDLGGASTQITFLPQFEXTLEQT 220

DB 63 KGSVSIMDSDEGILAWVTNFTVGLGHRQETVGTLDLGGASTQITFLPQFEXTLEQT 122

QY 221 PRGILTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETEGTDGHTFRSACLPRVLEAE 280

DB 123 PXGLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETEGTDGHTFRSACLPRVLEAE 182

QY 281 WIFGVVKYQXGNQGEVGFPCYAEVLRVVRGKLHQPVEVQVGSFYAFSYFYDRVTD 340

DB 183 WIFGVVKYQXGNQGEVGFPCYAEVLRVVRGKLHQPVEVQVGSFYAFSYFYDRVTD 242

QY 341 MIDYKGGILKVDFFERKAREVCNDLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQ 400

DB 243 MIDYKGGILKVDFFERKAREVCNDLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQ 302

QY 401 LTKVNNIETGKMGALGATFHLQSLGISH 428

DB 303 LTKVNNIETGKMGALGATFHLQSLGISH 330

RESULT 15

US-10-286-926-27
 ; Sequence 27, Application US/10286926
 ; Publication No. US20030175752A1
 ; GENERAL INFORMATION:

APPLICANT: Mulero, John

APPLICANT: Yung, George

APPLICANT: Mulero, Julio

APPLICANT: Yung, George

APPLICANT: Mulero, Julio

FILE REFERENCE: 28110/36457CON

TITLE OF INVENTION: Methods and Materials Relating to CD39-Like

FILE REFERENCE: 28110/36457CON

CURRENT FILING DATE: 2002-11-01

PRIOR FILING DATE: 2002-11-01

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-01-11

PRIOR FILING DATE: 2000-01-11

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-07-16

PRIOR FILING DATE: 1999-07-16

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-03-19

PRIOR FILING DATE: 1999-03-19

PRIOR FILING DATE: 1998-07-24

PRIOR FILING DATE: 1998-07-24

PRIOR FILING DATE: 1999-02-04

PRIOR FILING DATE: 1999-02-04

PRIOR FILING DATE: 1998-07-16

PRIOR FILING DATE: 1998-07-16

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 27

LENGTH: 484

TYPE: PRT

ORGANISM: Homo sapiens

US-10-286-926-27

Query Match 44.4%; Score 999; DB 12; Length 484;

Best Local Similarity 52.4%; Pred. No. 1.1e-90;

Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;

QY 40 PINVSA---STLYGIMFDAGSTGTHVYTFVQMPGOLPILEGVEFSDSVKPGLSAFVDQ 96

DB 90 PLGTAADGHEVYGYIMFDAGSTGTHVYTFVQMPGOLPILEGVEFSDSVKPGLSAFVDQ 148

QY 97 PKQGAETVOGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSPL 156

DB 149 VEKSAQGIIRRELDVAKQDIPDFWKATPLVLKATAGLRLLPEHKAKALLFEVKEIFRKSPL 208

QY 157 FLVPRKGSVIMDSDEGILAWVTNFTVGLGHRQETVGTLDLGGASTQITFLPQFEXT 216

DB 209 FLVGGDCVSINNGTDEGVSAITINFTGLSKTFCGSSVGMWLDLGGASTQIAFLPRVEGT 268

QY 217 LQOTFRGILTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETEGTDGHTFRSACLPR 275

DB 269 LQASPPGYLTALRMFNRTYKLYSYLGLGMSARLATLGGVGGQPKADGKELVSPCLSP 328

QY 276 WLEAEWIFGVVKYQXGNQGEVGFPCYAEVLRVVRGKLHQPVEVQVGSFYAFSYFYDR 335

DB 329 SPKGEWEHAEVTVRVSQKAAALHELCAARVSEVLQNRVHRTEEVKGVDFYAFSYFYDR 388

QY 336 AVDTMIDYKGGILKVDFFERKAREVCNDLENFTSGSPFLCMLDSYITALLKDGFGFAD 395

DB 389 AAGVGLIDAEKGGISLVGDFEIAAKYVCRITLETQFQSPSPSCMDLTYVSLILOE-FGFPR 447

QY 396 STVLQTLTKVNNIETGKMGALGATFHLQSL 424

DB 448 SKVLKLTTRKIDNVEISWALGAIFHYIDSL 476

Thu Nov 13 06:30:34 2003

us-09-905-744b-6.rapb

Page 9

Search completed: November 13, 2003, 06:26:02
Job time : 45 secs

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OM protein - protein search, using sw model

Run on: November 13, 2003, 06:17:36 ; Search time 21 Seconds
(without alignments)
862.336 Million cell updates/sec

Title: US-09-905-744B-6
Perfect score: 2250
Sequence: 1 MATSWGTVFFMLVSCVCSA.....ETGWLGAATHLLQSLGISH 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pap:*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pap:*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pap:*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pap:*
5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pap:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2250	100.0	428	4	US-09-608-285A-3
2	2250	100.0	428	4	US-09-608-285A-5
3	2250	100.0	428	4	US-09-240-639-6
4	2250	100.0	428	4	US-09-240-639-9
5	2250	100.0	428	4	US-09-350-836B-3
6	2250	100.0	428	4	US-09-350-836B-5
7	2250	100.0	428	4	US-09-370-265-3
8	2250	100.0	428	4	US-09-370-265-5
9	2250	100.0	428	4	US-09-557-800C-3
10	2250	100.0	428	4	US-09-557-800C-5
11	2235	99.3	428	4	US-09-608-285A-7
12	2235	99.3	428	4	US-09-350-836B-7
13	2235	99.3	428	4	US-09-370-265-7
14	2235	99.3	428	4	US-09-557-800C-7
15	2104	93.5	405	4	US-09-608-285A-25
16	2104	93.5	405	4	US-09-370-265-25
17	2104	93.5	405	4	US-09-557-800C-25
18	1837.5	81.7	465	4	US-09-557-800C-56
19	1832.5	81.4	465	4	US-09-240-639-8
20	999	44.4	456	4	US-09-240-639-2
21	999	44.4	484	4	US-09-608-285A-27
22	999	44.4	484	4	US-09-370-265-27
23	999	44.4	484	4	US-09-557-800C-27
24	819.5	36.4	471	4	US-09-608-285A-60
25	507.5	22.6	459	4	US-09-129-112-9
26	503.5	22.4	467	4	US-09-129-112-19
27	498	22.1	462	4	US-09-129-112-2

28	491.5	21.8	462	4	US-09-129-112-15	Sequence 15, Appl
29	489	21.7	455	4	US-09-240-639-10	Sequence 10, Appl
30	467.5	20.8	473	4	US-09-240-639-12	Sequence 12, Appl
31	446.5	19.8	454	4	US-09-240-639-11	Sequence 11, Appl
32	351	15.6	502	4	US-09-557-800C-55	Sequence 55, Appl
33	351	15.6	510	3	US-08-930-921-1	Sequence 1, Appl
34	347.5	15.4	529	4	US-09-240-639-4	Sequence 4, Appl
35	234	10.4	148	4	US-09-240-639-17	Sequence 17, Appl
36	186	8.3	153	4	US-09-240-639-13	Sequence 16, Appl
37	180.5	8.0	150	4	US-09-240-639-16	Sequence 15, Appl
38	179	8.0	153	4	US-09-240-639-15	Sequence 14, Appl
39	174	7.7	154	4	US-09-240-639-14	Sequence 13, Appl
40	106.5	4.7	553	1	US-08-565-386-12	Sequence 20854, A
41	105.5	4.7	339	4	US-09-252-991A-20854	Sequence 2, Appl
42	98.5	4.4	535	3	US-09-137-077-2	Sequence 4383, Ap
43	96	4.3	506	4	US-09-134-001C-4383	Sequence 2, Appl
44	93	4.1	969	2	US-08-284-941-2	Sequence 2, Appl
45	93	4.1	969	2	US-08-447-642-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-608-285A-3
; Sequence 3, Application US/09608285A
; Patent No. 635013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-285A-3

Query Match 100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred.No. 3.9e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MATSWGTVFFMLVSCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGINFADAGSTGT	60
Qy	61	RHIVTVQKMPGQLPILEGEVDFSVKPGLSAFVDPQKQGAETVQGLLEAVKDSIPRSHW	120

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        |||
Db      121  KKTTPVVKATAGLRLPEHKAKALLFEVKEIFRKSFLVPKGSVIMDSDEGILLAWTV 180
        |||
Qy      181  NFLTQGLHGRQETVGTDLGGASTQITFLPQPEKTELEOTPRGYLTSFEMFNSTYKLYTH 240
        |||
Db      181  NFLTQGLHGRQETVGTDLGGASTQITFLPQPEKTELEOTPRGYLTSFEMFNSTYKLYTH 240
        |||
Qy      241  SYLGFGGLKAARLATLGALETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGNQGEVGF 300
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Db      241  SYLGFGGLKAARLATLGALETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGNQGEVGF 300
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Qy      301  EPCVAEVLVRVVRGKLHQPVEVQSGFVAFSYYYDRAVDMDIDYERKGGILKVEDFERKAR 360
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Db      301  EPCVAEVLVRVVRGKLHQPVEVQSGFVAFSYYYDRAVDMDIDYERKGGILKVEDFERKAR 360
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Qy      361  EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGVALGATPHL 420
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Db      361  EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGVALGATPHL 420
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Qy      421  LQSLGISH 428
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Db      421  LQSLGISH 428
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RESULT 2

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US-09-608-285A-5
; Sequence 5, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-10
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-285A-5

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Query Match      100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 3,9e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61  RIHYVTFVQKMPQOLPILEGEVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
        |||
Qy      121  KKTTPVVKATAGLRLPEHKAKALLFEVKEIFRKSFLVPKGSVIMDSDEGILLAWTV 180
        |||
Db      121  KKTTPVVKATAGLRLPEHKAKALLFEVKEIFRKSFLVPKGSVIMDSDEGILLAWTV 180
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Qy      181  NFLTQGLHGRQETVGTDLGGASTQITFLPQPEKTELEOTPRGYLTSFEMFNSTYKLYTH 240
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Db      181  NFLTQGLHGRQETVGTDLGGASTQITFLPQPEKTELEOTPRGYLTSFEMFNSTYKLYTH 240
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Qy      241  SYLGFGGLKAARLATLGALETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGNQGEVGF 300
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Db      241  SYLGFGGLKAARLATLGALETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGNQGEVGF 300
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Qy      301  EPCVAEVLVRVVRGKLHQPVEVQSGFVAFSYYYDRAVDMDIDYERKGGILKVEDFERKAR 360
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Db      301  EPCVAEVLVRVVRGKLHQPVEVQSGFVAFSYYYDRAVDMDIDYERKGGILKVEDFERKAR 360
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Qy      361  EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGVALGATPHL 420
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Db      361  EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGVALGATPHL 420
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Qy      421  LQSLGISH 428
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Db      421  LQSLGISH 428
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RESULT 3

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US-09-240-639-6
; Sequence 6, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-6

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Query Match      100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 3,9e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61  RIHYVTFVQKMPQOLPILEGEVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
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Qy      121  KKTTPVVKATAGLRLPEHKAKALLFEVKEIFRKSFLVPKGSVIMDSDEGILLAWTV 180
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Db      121  KKTTPVVKATAGLRLPEHKAKALLFEVKEIFRKSFLVPKGSVIMDSDEGILLAWTV 180
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Qy      181  NFLTQGLHGRQETVGTDLGGASTQITFLPQPEKTELEOTPRGYLTSFEMFNSTYKLYTH 240
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Db      181  NFLTQGLHGRQETVGTDLGGASTQITFLPQPEKTELEOTPRGYLTSFEMFNSTYKLYTH 240
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DB 241 SYLGFLKAARLATLGALETGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
QY 301 EPCYAEVLVRGKLHQPEEVRGSGFYAFSYDDRAVDMDIDYEKGKILKVEDFERKAR 360
DB 301 EPCYAEVLVRGKLHQPEEVRGSGFYAFSYDDRAVDMDIDYEKGKILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTKKVNNIETGHWALGATPHL 420
DB 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTKKVNNIETGHWALGATPHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 4
US-09-240-639-9
; Sequence 9, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-9

Query Match 100.0%; Score 2250; DB 4; Length 428;
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Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 RIHVYTFVQKMPQQLPILEGVEFDSVKPGLSAFVDPQKGAETVQGLLVAKDSIPRSHW 120
QY 121 KKTVPVLKATAGRLLLPEHAKALLFEVKEIFRKSPLVPKGSVIMDSDEGILAWVTV 180
DB 121 KKTVPVLKATAGRLLLPEHAKALLFEVKEIFRKSPLVPKGSVIMDSDEGILAWVTV 180
QY 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQEKLTLEQTPRGYLTSEFMFNSTYKLYTH 240
DB 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQEKLTLEQTPRGYLTSEFMFNSTYKLYTH 240
QY 241 SYLGFLKAARLATLGALETGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
DB 241 SYLGFLKAARLATLGALETGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
QY 301 EPCYAEVLVRGKLHQPEEVRGSGFYAFSYDDRAVDMDIDYEKGKILKVEDFERKAR 360
DB 301 EPCYAEVLVRGKLHQPEEVRGSGFYAFSYDDRAVDMDIDYEKGKILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTKKVNNIETGHWALGATPHL 420
DB 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTKKVNNIETGHWALGATPHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 5
US-09-350-836B-3
; Sequence 3, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Mulero, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-836B-3

Query Match 100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.9e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MATSWGTFFVFMVWSCVSAVSHRNQQTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVQKMPQQLPILEGVEFDSVKPGLSAFVDPQKGAETVQGLLVAKDSIPRSHW 120
DB 61 RIHVYTFVQKMPQQLPILEGVEFDSVKPGLSAFVDPQKGAETVQGLLVAKDSIPRSHW 120
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DB 301 EPCYAEVLVRGKLHQPEEVRGSGFYAFSYDDRAVDMDIDYEKGKILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTKKVNNIETGHWALGATPHL 420
DB 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTKKVNNIETGHWALGATPHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 6
US-09-350-836B-5
; Sequence 5, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Mulero, John
; APPLICANT: Mulero, Julio

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; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-836B-5

Query Match      100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.9e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MATSWGTFFVFMVWSCVCSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60

Qy 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

Qy 121 KKTVPVLKATAGLRLPEHKAALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180
Db 121 KKTVPVLKATAGLRLPEHKAALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180

Qy 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQPEKLEQTPRGVLTSEFMENSTYKLYTH 240
Db 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQPEKLEQTPRGVLTSEFMENSTYKLYTH 240

Qy 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGVF 300
Db 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGVF 300

Qy 301 EPCYAEVLVRVVRGKLHQPEEVQVRSFYAFSYIYDRAVDTDMDIYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVVRGKLHQPEEVQVRSFYAFSYIYDRAVDTDMDIYKGGILKVEDFERKAR 360

Qy 361 EVCDNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGALGATFHL 420
Db 361 EVCDNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGALGATFHL 420

Qy 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 7
US-09-370-265-3
; Sequence 3, Application US/09370265
; Patent No. 644771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
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; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-265-3

Query Match      100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.9e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MATSWGTFFVFMVWSCVCSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60

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Db 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

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Db 121 KKTVPVLKATAGLRLPEHKAALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180

Qy 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQPEKLEQTPRGVLTSEFMENSTYKLYTH 240
Db 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQPEKLEQTPRGVLTSEFMENSTYKLYTH 240

Qy 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGVF 300
Db 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGVF 300

Qy 301 EPCYAEVLVRVVRGKLHQPEEVQVRSFYAFSYIYDRAVDTDMDIYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVVRGKLHQPEEVQVRSFYAFSYIYDRAVDTDMDIYKGGILKVEDFERKAR 360

Qy 361 EVCDNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGALGATFHL 420
Db 361 EVCDNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGALGATFHL 420

Qy 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 8
US-09-370-265-5
; Sequence 5, Application US/09370265
; Patent No. 644771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
```

EARLIER FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 09/122,449
EARLIER FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: 09/244,444
EARLIER FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 428
TYPE: PRT
ORGANISM: Homo sapiens
US-09-370-265-5

Query Match 100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.9e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSGTGFVFLVSCVSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSGTGFVFLVSCVSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVOKMPGQLPILGEVFDVSKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVOKMPGQLPILGEVFDVSKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTVPVLKATAGLRLPEHKAKALLFEVKEIFRKSPPFLVPKGSVSIIMDSDEGILAWTV 180
DB 121 KKTVPVLKATAGLRLPEHKAKALLFEVKEIFRKSPPFLVPKGSVSIIMDSDEGILAWTV 180
QY 181 NLTGQLHGHRETGTDLGGASTQITFLPQFKTLTQTPRGYLTSPMFNSTYKLYTH 240
DB 181 NLTGQLHGHRETGTDLGGASTQITFLPQFKTLTQTPRGYLTSPMFNSTYKLYTH 240
QY 241 SYLGFGLKAARLTLGALTEGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
DB 241 SYLGFGLKAARLTLGALTEGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
QY 301 EPCYAEVLVRVGRKHLQHPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKHLQHPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNDLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKNNIETGALCATPHL 420
DB 361 EVCNDLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKNNIETGALCATPHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 9
US-09-557-800C-3
Sequence 3, Application US/09557800C
Patent No. 6476211
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
FILE REFERENCE: 28110/36457
CURRENT APPLICATION NUMBER: US/09/557,800C
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273447

EARLIER FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 09/122,449
EARLIER FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: 09/244,444
EARLIER FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 428
TYPE: PRT
ORGANISM: Homo sapiens
US-09-370-265-5

Query Match 100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.9e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSGTGFVFLVSCVSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSGTGFVFLVSCVSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVOKMPGQLPILGEVFDVSKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVOKMPGQLPILGEVFDVSKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTVPVLKATAGLRLPEHKAKALLFEVKEIFRKSPPFLVPKGSVSIIMDSDEGILAWTV 180
DB 121 KKTVPVLKATAGLRLPEHKAKALLFEVKEIFRKSPPFLVPKGSVSIIMDSDEGILAWTV 180
QY 181 NLTGQLHGHRETGTDLGGASTQITFLPQFKTLTQTPRGYLTSPMFNSTYKLYTH 240
DB 181 NLTGQLHGHRETGTDLGGASTQITFLPQFKTLTQTPRGYLTSPMFNSTYKLYTH 240
QY 241 SYLGFGLKAARLTLGALTEGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
DB 241 SYLGFGLKAARLTLGALTEGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
QY 301 EPCYAEVLVRVGRKHLQHPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKHLQHPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNDLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKNNIETGALCATPHL 420
DB 361 EVCNDLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKNNIETGALCATPHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 9
US-09-557-800C-3
Sequence 3, Application US/09557800C
Patent No. 6476211
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
FILE REFERENCE: 28110/36457
CURRENT APPLICATION NUMBER: US/09/557,800C
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273447

; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/24444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-800C-5

Query Match 100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.9e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MATSGTGVFVFLVVCVCSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSGTGVFVFLVVCVCSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHVYTFVQKMPGQLPILGEGVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHVYTFVQKMPGQLPILGEGVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Qy 121 KKTVPVVKATAGLRLPEHKAALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180
Db 121 KKTVPVVKATAGLRLPEHKAALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180
Qy 181 NFLTGLQHGHRQETVGTLDLGGASTQITFLPQFEKTELEOTPRGYLTSPFEMFNSTYKLYTH 240
Db 181 NFLTGLQHGHRQETVGTLDLGGASTQITFLPQFEKTELEOTPRGYLTSPFEMFNSTYKLYTH 240
Qy 241 SYLGFLGKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVF 300
Db 241 SYLGFLGKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVF 300
Qy 301 EPCYAEVLVRVGRKHOPEEVQVQSGSFYAFSYVDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVGRKHOPEEVQVQSGSFYAFSYVDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTCKVNNIETGVALGATFHL 420
Db 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTCKVNNIETGVALGATFHL 420
Qy 421 LOSLGISH 428
Db 421 LOSLGISH 428

RESULT 11
US-09-608-285A-7
; Sequence 7, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09

; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-285A-7

Query Match 99.3%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 2e-246;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MATSGTGVFVFLVVCVCSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSGTGVFVFLVVCVCSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHVYTFVQKMPGQLPILGEGVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHVYTFVQKMPGQLPILGEGVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Qy 121 KKTVPVVKATAGLRLPEHKAALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180
Db 121 KKTVPVVKATAGLRLPEHKAALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180
Qy 181 NFLTGLQHGHRQETVGTLDLGGASTQITFLPQFEKTELEOTPRGYLTSPFEMFNSTYKLYTH 240
Db 181 NFLTGLQHGHRQETVGTLDLGGASTQITFLPQFEKTELEOTPRGYLTSPFEMFNSTYKLYTH 240
Qy 241 SYLGFLGKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVF 300
Db 241 SYLGFLGKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVF 300
Qy 301 EPCYAEVLVRVGRKHOPEEVQVQSGSFYAFSYVDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVGRKHOPEEVQVQSGSFYAFSYVDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTCKVNNIETGVALGATFHL 420
Db 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTCKVNNIETGVALGATFHL 420
Qy 421 LOSLGISH 428
Db 421 LOSLGISH 428

RESULT 12
US-09-350-836B-7
; Sequence 7, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16

;; PRIOR APPLICATION NUMBER: 09/122,449
;; PRIOR FILING DATE: 1998-07-24
;; PRIOR APPLICATION NUMBER: 09/244,444
;; PRIOR FILING DATE: 1999-02-04
;; NUMBER OF SEQ ID NOS: 23
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 7
;; LENGTH: 428
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-350-836B-7

Query Match 99.3%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 2e-246;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATSNGTVFFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSNGTVFFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDPQKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDPQKQGAETVQGLLEVAKDSIPRSHW 120

QY 121 KKTVPVLKATAGLRLLPEHKAKALLFEVKEIFRKSPLVPKGSVSIMDGSDEGILAWTV 180
DB 121 KKTVPVLKATAGLRLLPEHKAKALLFEVKEIFRKSPLVPKGSVSIMDGSDEGILAWTV 180

QY 181 NFLTGQHGHRQETVGTLDLGGASTQITFLPQFEXTLEOTPRGYLTSEMFNSTYKLYTH 240
DB 181 NFLTGQHGHRQETVGTLDLGGASTQITFLPQFEXTLEOTPRGYLTSEMFNSTYKLYTH 240

QY 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYCGNQEVEGF 300
DB 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYCGNQEVEGF 300

QY 301 EPCYAEVLVRVGRKHLQHOPEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKHLQHOPEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360

QY 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTKKVNNIETGALCATPHL 420
DB 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTKKVNNIETGALCATPHL 420

QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 13
US-09-370-265-7
;; Sequence 7, Application US/09370265
;; Patent No. 6447771
;; GENERAL INFORMATION:
;; APPLICANT: Ford, John
;; APPLICANT: Mulero, Julio
;; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
;; FILE REFERENCE: 28111/35908
;; CURRENT APPLICATION NUMBER: US/09/370,265
;; PRIOR FILING DATE: 1999-08-09
;; EARLIER APPLICATION NUMBER: PCT/US99/16180
;; EARLIER FILING DATE: 1999-07-16
;; EARLIER APPLICATION NUMBER: 09/350,836
;; EARLIER FILING DATE: 1999-07-09
;; EARLIER APPLICATION NUMBER: 09/273,447
;; EARLIER FILING DATE: 1999-03-19
;; EARLIER APPLICATION NUMBER: 09/244,444
;; EARLIER FILING DATE: 1999-02-04
;; EARLIER APPLICATION NUMBER: 09/122,449
;; EARLIER FILING DATE: 1998-07-24
;; EARLIER APPLICATION NUMBER: 09/118,205
;; EARLIER FILING DATE: 1998-07-16

;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 7
;; LENGTH: 428
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-370-265-7

Query Match 99.3%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 2e-246;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATSNGTVFFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSNGTVFFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDPQKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDPQKQGAETVQGLLEVAKDSIPRSHW 120

QY 121 KKTVPVLKATAGLRLLPEHKAKALLFEVKEIFRKSPLVPKGSVSIMDGSDEGILAWTV 180
DB 121 KKTVPVLKATAGLRLLPEHKAKALLFEVKEIFRKSPLVPKGSVSIMDGSDEGILAWTV 180

QY 181 NFLTGQHGHRQETVGTLDLGGASTQITFLPQFEXTLEOTPRGYLTSEMFNSTYKLYTH 240
DB 181 NFLTGQHGHRQETVGTLDLGGASTQITFLPQFEXTLEOTPRGYLTSEMFNSTYKLYTH 240

QY 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYCGNQEVEGF 300
DB 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYCGNQEVEGF 300

QY 301 EPCYAEVLVRVGRKHLQHOPEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKHLQHOPEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360

QY 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTKKVNNIETGALCATPHL 420
DB 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTKKVNNIETGALCATPHL 420

QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 14
US-09-557-800C-7
;; Sequence 7, Application US/09557800C
;; Patent No. 6476211
;; GENERAL INFORMATION:
;; APPLICANT: Ford, John
;; APPLICANT: Mulero, Julio
;; APPLICANT: Yeung, George
;; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
;; FILE REFERENCE: 28110/36457
;; CURRENT APPLICATION NUMBER: US/09/557,800C
;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: 09/481,238
;; PRIOR FILING DATE: 2000-01-11
;; PRIOR APPLICATION NUMBER: 09/370,265
;; PRIOR FILING DATE: 1999-08-09
;; PRIOR APPLICATION NUMBER: PCT/US99/16180
;; PRIOR FILING DATE: 1999-07-16
;; PRIOR APPLICATION NUMBER: 09/350836
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: 09/273447
;; PRIOR FILING DATE: 1999-03-19
;; PRIOR APPLICATION NUMBER: 09/122449
;; PRIOR FILING DATE: 1998-07-24
;; PRIOR APPLICATION NUMBER: 09/244444
;; PRIOR FILING DATE: 1999-02-04
;; PRIOR APPLICATION NUMBER: 09/118,205

;; PRIOR FILING DATE: 1998-07-16
;; NUMBER OF SEQ ID NOS: 56
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 7
;; LENGTH: 428
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-557-800C-7

Query Match 99.3%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 2e-246;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATSWGTVFFMLVWSCVCSAVSHRNQQTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVFFMLVWSCVCSAVSHRNQQTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVQKMPQQLPILEGVDSVKPGLSAFVDQPKQGAETVQGLLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKMPQQLPILEGVDSVKPGLSAFVDQPKQGAETVQGLLLEVAKDSIPRSHW 120
QY 121 KKTVPVLKATAGLRLPEHKAKALLFEVKEIFPKSPFLVPKGSVSMDSDEGILAWTV 180
DB 121 KKTVPVLKATAGLRLPEHKAKALLFEVKEIFPKSPFLVPKGSVSMDSDEGILAWTV 180
QY 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEKTLQTPRGYLTSEMFNSTYKLYTH 240
DB 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEKTLQTPRGYLTSEMFNSTYKLYTH 240
QY 241 SYLGFGKLAARLATALGALETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
DB 241 SYLGFGKLAARLATALGALETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
QY 301 EPCYAEVLVRVGRKHLQPEVQSGSFYAFSYVYDRAVDTMDIDYEKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKHLQPEVQSGSFYAFSYVYDRAVDTMDIDYEKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKVANNIETGMALGATFHL 420
DB 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKVANNIETGMALGATFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 15
US-09-608-285A-25
; Sequence 25, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19

;; PRIOR APPLICATION NUMBER: 09/244,444
;; PRIOR FILING DATE: 1999-02-04
;; PRIOR APPLICATION NUMBER: 09/122,449
;; PRIOR FILING DATE: 1998-07-24
;; PRIOR APPLICATION NUMBER: 09/118,205
;; PRIOR FILING DATE: 1998-07-16
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 25
;; LENGTH: 405
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-608-285A-25

Query Match 93.5%; Score 2104; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 1.7e-231;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSWGTVFFMLVWSCVCSAVSHRNQQTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVFFMLVWSCVCSAVSHRNQQTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVQKMPQQLPILEGVDSVKPGLSAFVDQPKQGAETVQGLLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKMPQQLPILEGVDSVKPGLSAFVDQPKQGAETVQGLLLEVAKDSIPRSHW 120
QY 121 KKTVPVLKATAGLRLPEHKAKALLFEVKEIFPKSPFLVPKGSVSMDSDEGILAWTV 180
DB 121 KKTVPVLKATAGLRLPEHKAKALLFEVKEIFPKSPFLVPKGSVSMDSDEGILAWTV 180
QY 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEKTLQTPRGYLTSEMFNSTYKLYTH 240
DB 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFEKTLQTPRGYLTSEMFNSTYKLYTH 240
QY 241 SYLGFGKLAARLATALGALETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
DB 241 SYLGFGKLAARLATALGALETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
QY 301 EPCYAEVLVRVGRKHLQPEVQSGSFYAFSYVYDRAVDTMDIDYEKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKHLQPEVQSGSFYAFSYVYDRAVDTMDIDYEKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ 400
DB 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ 400

Search completed: November 13, 2003, 06:24:36
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 13, 2003, 06:08:47 ; Search time 18 Seconds
(without alignments)
1118.191 Million cell updates/sec

Title: US-09-905-744B-6
Perfect score: 2250
Sequence: 1 MATSWGVFVFLVVCVCSA.....ETGALGATFHLLQSLGISH 428

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2250	100.0	428	1 ENP5 HUMAN	O75356 homo sapien
2	1994.5	88.6	427	1 ENP5 MOUSE	O9wuz9 mus musculus
3	1933.5	85.9	469	1 ENP5 MESAU	O9wvcs mesocricetu
4	999	44.4	484	1 ENP6 HUMAN	O75354 homo sapien
5	986	43.8	455	1 ENP6 RAT	O9erj1 rattus norv
6	489	21.7	455	1 NTPA PEA	P52914 pisum sativ
7	483.5	21.5	518	1 GDA1 YEAST	P32621 saccharomyc
8	446.5	19.8	454	1 APY SOLTU	P80595 solanum tub
9	387.5	17.2	485	1 VY4E CABEL	O18411 caenorhabdi
10	385	17.1	552	1 VY4E CABEL	O21815 caenorhabdi
11	383	17.0	493	1 ENP1 CHICK	O93295 gallus gall
12	372	16.5	630	1 YND1 YEAST	P40093 saccharomyc
13	370	16.4	510	1 ENP1 MOUSE	P55772 mus musculus
14	365	16.2	513	1 ENP1 BOVIN	O18956 bos taurus
15	360.5	16.0	613	1 ENP4 MOUSE	O9dbt4 mus musculus
16	357	15.9	616	1 ENP4 HUMAN	O9v227 homo sapien
17	352	15.6	510	1 ENP1 PIG	O9mvt4 sus scrofa
18	351	15.6	510	1 ENP1 HUMAN	P42961 homo sapien
19	348.5	15.5	511	1 ENP1 RAT	P97687 rattus norv
20	347.5	15.4	529	1 ENP3 HUMAN	O75355 homo sapien
21	339.5	15.1	495	1 ENP2 HUMAN	O9y513 homo sapien
22	309.5	13.8	495	1 ENP2 MOUSE	O55036 mus musculus
23	302.5	13.4	494	1 ENP2 RAT	O35795 rattus norv
24	301.5	13.4	495	1 ENP2 CHICK	P79784 gallus gall
25	140	6.2	628	1 NTP1 TOXGO	O27893 toxoplasma
26	138	6.1	628	1 NTP2 TOXGO	O27895 toxoplasma
27	131	5.8	592	1 NTP4 TOXGO	P52913 toxoplasma
28	111.5	5.0	634	1 SELB MOOTH	O46455 moorella th
29	106.5	4.7	553	1 VGI SPV4	P11333 spiroplasma
30	104.5	4.6	4427	1 PKSL BACSU	O05470 bacillus su
31	101.5	4.5	1151	1 Y245 TREPA	O83273 treponema p
32	99.5	4.4	535	1 DEXB STREN	O34796 streptococc
33	99.5	4.4	548	1 THER_BACST	P06874 bacillus st

RESULT 1

ENP5_HUMAN

ID

ENP5_HUMAN

STANDARD;

PRT; 428 AA.

AC

O75356;

DT

16-OCT-2001

(Rel. 40, Created)

DT

16-OCT-2001

(Rel. 40, Last sequence update)

DT

16-OCT-2001

(Rel. 40, Last annotation update)

DE

Ectonucleoside triphosphate diphosphohydrolase 5 precursor

DE

(EC 3.6.1.6) (NTPDases) (Nucleoside diphosphatase) (CD39 antigen-like

DE

4) (ER-UDPase).

GN

ENTPD5 OR CD39L4.

OS

Homo sapiens (Human).

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX

NCBI_TaxID=9606;

RN

[1]

RP

SEQUENCE FROM N.A.

RC

TISSUE=Leukemia;

RX

MEDLINE=98341119; PubMed=9676430;

RA

Chadwick B.P., Frischauf A.-M.;

RT

"The CD39-like gene family: identification of three new human members

RT

(CD39L2, CD39L3, and CD39L4); their murine homologues, and a member of

RT

the gene family from Drosophila melanogaster.";

RL

Genomics 50:357-367(1998).

CC

-!- FUNCTION: LIKELY TO PROMOTE REGLYCOSYLATION REACTIONS INVOLVED IN

CC

GLYCOPROTEINS FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC

CC

RETICULUM. HYDROLYZES UDP, GDP AND IDP BUT NOT ANY OTHER

CC

NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES, NOR THIAMINE PYROPHOSPHATE

CC

(BY SIMILARITY).

CC

-!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a

CC

nucleotide + phosphate.

CC

-!- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.

CC

-!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).

CC

-!- TISSUE SPECIFICITY: EXPRESSED IN ADULT LIVER, KIDNEY, PROSTATE,

CC

TESTIS AND COLON. MUCH WEAKER EXPRESSION IN OTHER TISSUES.

CC

-!- SIMILARITY: BELONGS TO THE GDAI / CD39 NTPASE FAMILY.

CC

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CC

EMBL; AF039918; AAC39885.1; -

CC

Genew; HGNC:3367; ENTPD5.

CC

MIM: 603162; -

CC

CO; G01004002; Fadenosinetriphosphatase activity; TAS.

CC

InterPro; IPR000407; GDAI_CD39_NTPase.

CC

Pfam; PF01150; GDAI_CD39; 1.

CC

PROSITE; PS01238; GDAI_CD39_NTPASE; FALSE NEG.

CC

KW Hydroxylase; Transmembrane; Glycoprotein; Calcium; Magnesium;

CC

Endoplasmic reticulum; Signal.

CC

FT SIGNAL 1 20 POTENTIAL.

CC

CHAIN 21 428 ECTONUCLEOSIDE TRIPHOSPHATE

CC

FT

CHAIN 21 428 ECTONUCLEOSIDE TRIPHOSPHATE

CC

FT

CHAIN 21 428 ECTONUCLEOSIDE TRIPHOSPHATE

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FT

CHAIN 21 428 ECTONUCLEOSIDE TRIPHOSPHATE

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CHAIN 21 428 ECTONUCLEOSIDE TRIPHOSPHATE

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CHAIN 21 428 ECTONUCLEOSIDE TRIPHOSPHATE

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CHAIN 21 428 ECTONUCLEOSIDE TRIPHOSPHATE

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CHAIN 21 428 ECTONUCLEOSIDE TRIPHOSPHATE

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CHAIN 21 428 ECTONUCLEOSIDE TRIPHOSPHATE

CC

FT

CHAIN 21 428 ECTONUCLEOSIDE TRIPHOSPHATE

FT CARBOHYD 42 42 DIPHOSPHOHYDROLASE 5.
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 428 AA; 47517 MW; 830437A155DE4DDD CRC64;
 Query Match 100.0%; Score 2250; DB 1; Length 428;
 Best Local Similarity 100.0%; Pred. No. 3.3e-173; Indels 0; Gaps 0;
 Matches 428; Conservative 0; Mismatches 0;
 QY 1 MATSGTGVFFMLVWSCVCSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSGTGVFFMLVWSCVCSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 QY 61 RIHVTVFVKQPGQLPILGEVDSVKGLSAFVDQPKQAGTETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHVTVFVKQPGQLPILGEVDSVKGLSAFVDQPKQAGTETVQGLLEVAKDSIPRSHW 120
 QY 121 KKTVPVLKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMDSDEGILAWTV 180
 DB 121 KKTVPVLKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMDSDEGILAWTV 180
 QY 181 NFLTGLQGHQRTVGTLDLGSATQITFLQFQKTLQTPRGVLTSPFEMFNSTYKLYTH 240
 DB 181 NFLTGLQGHQRTVGTLDLGSATQITFLQFQKTLQTPRGVLTSPFEMFNSTYKLYTH 240
 QY 241 SYLFGGLKAARLATLGALETGTGHTPRSAFLRWLEAEVFGVYVQGNQGEVGF 300
 DB 241 SYLFGGLKAARLATLGALETGTGHTPRSAFLRWLEAEVFGVYVQGNQGEVGF 300
 QY 301 EPCVAELRVVRGKLHQPEEVQGSFVAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR 360
 DB 301 EPCVAELRVVRGKLHQPEEVQGSFVAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR 360
 QY 361 EVCNLENFTSGSPCLNDLSYITALLKDGFGFADSTVLTQKNNIETGALGATFHL 420
 DB 361 EVCNLENFTSGSPCLNDLSYITALLKDGFGFADSTVLTQKNNIETGALGATFHL 420
 QY 421 LQSLGISH 428
 DB 421 LQSLGISH 428

RESULT 2

ENP5 MOUSE STANDARD; PRT; 427 AA.
 ID_Q9WU29; 070214; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Ectonucleoside triphosphate diphosphohydrolase 5 precursor
 DE (EC 3.6.1.6) (NTPDase5) (Nucleoside diphosphatase) (CD39 antigen-like
 DE 4) (ER-UDPase).
 GN ENTPD5 OR CD39L4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=98119025; PubMed=9457681;
 RA Chadwick B.P., Williamson J., Sheer D., Frischauf A.-M.;
 RT "cDNA cloning and chromosomal mapping of a mouse gene with homology to
 RT NTPases.";
 RL Mamm. Genome 9:162-164 (1998).
 RN (2)
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND CHARACTERIZATION.
 RC TISSUE=Liver;
 RX MEDLINE=99298181; PubMed=10369669;
 RA Trombetta E.S., Helenius A.;
 RT "Glycoprotein regucosylation and nucleotide sugar utilization in the
 RT secretory pathway: identification of a nucleoside diphosphatase in the

endoplasmic reticulum.";
 RL EMBO J. 18:3282-3292 (1999).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schram L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Blake J., Boffelli D., Bojunga N., Anon H., Baldarelli R., Barth G.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 CC -1- FUNCTION: LIKELY TO PROMOTE REGLYCOSYLATION REACTIONS INVOLVED IN
 CC GLYCOPROTEIN FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC
 CC RETICULUM. HYDROLYZES UDP, GDP AND IDP BUT NOT ANY OTHER
 CC NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES, NOR THIAMINE
 CC PYROPHOSPHATE.
 CC -1- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
 CC nucleotide + phosphate.
 CC -1- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -1- PTM: GLYCOSYLATED WITH HIGH MANNOSE N-LINKED GLYCANS.
 CC -1- MISCELLANEOUS: OPTIMAL pH IS NEUTRAL.
 CC -1- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
 CC
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 CC
 CC EMBL; AF006482; AAC05181.1; -
 CC ENBL; AJ238636; CB45833.1; -
 CC ENBL; AK002618; BAB22234.1; -
 CC MGD; MGI:1321385; Entpds.
 CC InterPro; IPR000407; GDA1_CD39_NTPase.
 CC Pfam; PF01150; GDA1_CD39; 1.
 CC PROSITE; PS01238; GDA1_CD39_NTPASE; FALSE NEG.
 CC Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
 CC Endoplasmic reticulum; Signal; POTENTIAL.
 FT SIGNAL 1 18
 FT CHAIN 19 427
 FT ECTONUCLEOSIDE TRIPHOSPHATE
 FT DIPHOSPHOHYDROLASE 5.
 FT CARBOHYD 41 41
 FT CARBOHYD 231 231
 FT CONFLICT 390 390
 FT CONFLICT 394 427
 FT DGTLLQTLKVNITETGALGATFHLGSLGITS -> ERH
 FT PLTAHKSSEQHRDWLGLGSHSPAPVSHHQHQRPSSTSEAC
 FT ISEPVFSQEGVDSSTETFSLSGKAWPETR (IN REF. 1).
 SQ SEQUENCE 427 AA; 47101 MW; 2F9DA2C342C55577 CRC64;
 Query Match 88.6%; Score 1994.5; DB 1; Length 427;
 Best Local Similarity 88.3%; Pred. No. 1.1e-152;
 Matches 377; Conservative 24; Mismatches 25; Indels 1; Gaps 1;
 QY 1 MATSGTGVFFMLVWSCVCSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60

1 MATSWGAV-FMLIIACVGVSTVFYREQQTWFGVFLSSMCPINVSAGTFYGINFEDAGSTGT 59
 61 RIHVYTFVQKMPGOLPILGEVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 60 RIHVYTFVQKTAQQLPFLGEIEFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 119
 121 KKTVPVVKATAGLRLPEHAKALLFEVKEIFPKSPFLPKGVSIMDSGDLAWTV 180
 120 ERTVPVVKATAGLRLPEHAKALLFEVKEIFPKSPFLPKGVSIMDSGDLAWTV 179
 181 NLTGQLHGRQETVGLDGGASTQITFLPQEKLEOTPRGYLTSFPMFNSTFKLYTH 240
 180 NLTGQLHGRQETVGLDGGASTQITFLPQEKLEOTPRGYLTSFPMFNSTFKLYTH 239
 241 SYLGFGKAAARLALTLGALETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
 240 SYLGFGKAAARLALTLGALETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 299
 301 EPCVAEVLVRVQKGLHQPVEVQSGSFVAFSYDDRAVDMDIYKGGILKVEDFERKAR 360
 300 EPCVAEVLVRVQKGLHQPVEVQSGSFVAFSYDDRAVDMDIYKGGILKVEDFERKAR 359
 361 EVCNMLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGALGATFHL 420
 360 EVCNMLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGALGATFHL 419
 421 LQSLGIS 427
 420 LQSLGIT 426

RESULT 3
 ENP6 MESAU STANDARD; PRT; 469 AA.
 AC Q9QY08; Q9QY09;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 5 precursor
 DE (EC 3.6.1.6) (NTPDase5) (Nucleoside diphosphatase) (CD39 antigen-like
 DE 4) (ER-UPase) (Proco-oncogene cph).
 GN ENTPD5 OR CD39L4 OR CPH.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99142925; PubMed=999819;
 RA Velasco J.A., Avila M.A., Notario V.;
 RT "The product of the cph oncogene is a truncated, nucleotide-binding
 RT protein that enhances cellular survival to stress."
 RL Oncogene 18:689-701(1999).
 CC -! FUNCTION: LIKELY TO PROMOTE REGLYCOSYLATION REACTIONS INVOLVED IN
 CC GLYCOPROTEIN FOLDING AND QUALITY CONTROL IN THE ENDOPLASMIC
 CC RETICULUM. HYDROLYZES UDP, GDP AND IDP BUT NOT ANY OTHER
 CC NUCLEOSIDE DI-, MONO- OR TRIPHOSPHATES, NOR THIAMINE PYROPHOSPHATE
 CC (BY SIMILARITY).
 CC -! CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
 CC nucleotide + phosphate.
 CC -! COFACTOR: REQUIRES CALCIUM AND MAGNESIUM (BY SIMILARITY).
 CC -! SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -! TISSUE SPECIFICITY: EXPRESSED IN FETAL CELLS AND MOST ADULT
 CC TISSUES.
 CC -! DISEASE: CPH ONCOGENE HAS TRANSFORMING CAPACITY AND TUMORIGENIC
 CC POTENTIAL.
 CC -! SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
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 EMBL; AF084568; AAF22931.1; ALT_TERM.
 EMBL; AF084569; AAF22932.1; .
 InterPro; IPR000407; GDA1_CD39_NTPase.
 Pfam; PF01150; GDA1_CD39; 1.
 PROSITE; PS01238; GDA_CD39_NTPASE; FALSE_NEG.
 KX Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium;
 KW Endoplasmic reticulum; Signal; Proto-oncogene.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 469 ECTONUCLEOSIDE TRIPHOSPHATE
 FT DIPOHOSPHOHYDROLASE 5.
 FT CARBOHYD 42 42 N-LINKED (GLCNAC:...) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC:...) (POTENTIAL).
 SQ SEQUENCE 469 AA; 52125 MW; 03DBA23B0C73474B CRC64;
 Query Match 85.9%; Score 1933.5; DB 1; Length 469;
 Best Local Similarity 86.7%; Pred. No. 9.8e-148;
 Matches 364; Conservative 22; Mismatches 31; Indels 3; Gaps 1;
 QY 1 MATSWGAVFVFLVSVCSAVSHRNQQTWFGVFLSSMCPINVSASTLYGIMFEDAGSTGT 60
 DB 1 MATPWGAVFVFLVSVCSAVSHRNQQTWFGVFLSSMCPANVSASTLYGIMFEDAGSTGT 60
 QY 61 RIHVYTFVQKMPGOLPILGEVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHVYTFVQKAAQQLPFLGEIEFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 QY 121 KKTVPVVKATAGLRLPEHAKALLFEVKEIFPKSPFLPKGVSIMDSGDLAWTV 180
 DB 121 KKTVPVVKATAGLRLPEHAKALLFEVKEIFPKSPFLPKGVSIMDSGDLAWTV 180
 QY 181 NLTGQLHGRQETVGLDGGASTQITFLPQEKLEOTPRGYLTSFPMFNSTFKLYTH 240
 DB 181 NLTGQLHGRQETVGLDGGASTQITFLPQEKLEOTPRGYLTSFPMFNSTFKLYTH 240
 QY 241 SYLGFGKAAARLALTLGALETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
 DB 241 SYLGFGKAAARLALTLGALETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
 QY 301 EPCVAEVLVRVQKGLHQPVEVQSGSFVAFSYDDRAVDMDIYKGGILKVEDFERKAR 360
 DB 301 EPCVAEVLVRVQKGLHQPVEVQSGSFVAFSYDDRAVDMDIYKGGILKVEDFERKAR 360
 QY 361 EVCNMLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGALGATFHL 420
 DB 361 EVCNMLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGALGATFHL 417
 RESULT 4
 ENP6 HUMAN STANDARD; PRT; 484 AA.
 AC O75354; O9UJDI;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Ectonucleoside triphosphate diphosphohydrolase 6 (EC 3.6.1.6)
 DE (NTPDase6) (CD39 antigen-like 2).
 GN ENTPD6 OR CD39L2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Keratinocytes;
 RX MEDLINE=98341119; PubMed=9676430;
 RA Chadwick B.P., Frischauf A.-M.;
 RT "The CD39-like gene family: identification of three new human members
 RT (CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of

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 CC -----

DR EMBL; AJ277748; CAC16598.1; ..
 DR InterPro; IPR000407; GDA1_CD39_NTPase.
 DR Pfam; PF01150; GDA1_CD39; 1.
 DR PROSITE; PS01238; GDA1_CD39_NTPase; FALSE NEG.
 DR Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium;
 KW Signal-anchor; Golgi stack.
 FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 13 32 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT POTENTIAL.
 FT DOMAIN 33 455 LUMENAL (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLNAC. .) (POTENTIAL).
 FT CARBOHYD 256 256 N-LINKED (GLNAC. .) (POTENTIAL).
 SQ SEQUENCE 455 AA; 49899 MW; 19A22E8BAE0F077B CRC64;

Query Match 43.8%; Score 986; DB 1; Length 455;
 Best Local Similarity 54.0%; Pred. No. 1.2e-71;
 Matches 204; Conservative 51; Mismatches 117; Indels 6; Gaps 5;

QY 49 YGIMFDAGSGTGRHIVYTFVQKVPQQLPILEGEVDSVKRGLSAFVDQKQGAETVQGLL 108
 DB 74 YGIMFDAGSGTGRHIVYTFVQKVPQQLPILEGEVDSVKRGLSAFVDQKQGAETVQGLL 108
 QY 109 EVAKDSIPRSHWKTTPVVKATAGLLPEHAKALLFEVKEIFRKSPELVPKGSYIMD 168
 DB 133 NVAKQHPIPYFWKATPELVKATAGLLPEHAKALLFEVKEIFRKSPELVPKGSYIMD 168
 QY 169 GSDEGILAWTVNVLFGQLHGRQETVGLDGGASTQITFLPQFEKTLQTPRGYLTSP 228
 DB 193 GTDEGVSAWITVNFGLSLKTPGSSGVMLDLGGSGTQITFLPRVEGTQLQASPGHLTAL 252
 QY 229 EMENSTYKLYTHSYLGLKAAKRLATLGALETGTDGHTFRACLPRLAEWIGGVK 287
 DB 253 QMFNRTFKLYSYLGLKAAKRLATLGALETGTDGHTFRACLPRLAEWIGGVK 287
 QY 288 YOYGGNQEGBVG-FEPYAEVLVVRGKLHQPVEVQSGFYAFSYYYDRAVDMDIYDK 346
 DB 313 YRISGGK-AVGLYELCASRVSEVLNKHRTAEAOHVDFYAFSYYYDRAVDMDIYDK 346
 QY 347 GGILKVEDPERKAREVCDNLENTSGSPFLCMDSLYTALLKDGFGFADSTVLQTKVYN 406
 DB 371 GGSLLVVGDFEIAKAYVCRLETQPPSSPFACMDLTYISLLHE-FGFGDGKVLKARKID 429
 QY 407 NIETGALGATPHLLQSL 424
 DB 430 NVETSWALCAIFHYIDSL 447

RESULT 6

ID NTPA_PEA
 AC P52974;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Nucleoside-triphosphatase (EC 3.6.1.15) (Nucleoside triphosphate
 OS phosphohydrolase) (NTPase) (Apyrase).
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Alaska; TISSUE=Plumule;
 RX MEDLINE=96197404; PubMed=8616230;
 RA Hsieh H., Tong C.G., Thomas C., Roux S.J.;

RT "Light-modulated abundance of an mRNA encoding a calmodulin-regulated,
 RT chromatin-associated NTPase in pea.";
 RL Plant Mol. Biol. 30:135-147 (1996).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Alaska; TISSUE=Stem;
 RA Shibata K., Abe S., Davies E.;
 RT "Structure of the coding region and mRNA variants of the apyrase from
 RT Pisum sativum.";
 RL Acta Physiol. Plant. 20:3-13 (2001).

CC -!- FUNCTION: MIGHT BE INVOLVED IN RNA TRANSPORT OUT OF NUCLEI.
 CC -!- CATALYTIC ACTIVITY: NTP + H(2)O = NDP + phosphate.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.

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 CC -----

DR EMBL; Z32743; CAA83655.1; ..
 DR EMBL; AB027614; BAB18900.1; ..
 DR PIR; S65147; S48859.
 DR InterPro; IPR000407; GDA1_CD39_NTPase.
 DR Pfam; PF01150; GDA1_CD39; 1.
 DR PROSITE; PS01238; GDA1_CD39_NTPase; 1.
 KW Hydrolyase; Nuclear protein.
 SQ SEQUENCE 455 AA; 50072 MW; 50FDF0023ABC4299 CRC64;

Query Match 21.7%; Score 489; DB 1; Length 455;
 Best Local Similarity 33.7%; Pred. No. 1e-31;
 Matches 140; Conservative 62; Mismatches 160; Indels 54; Gaps 14;

QY 49 YGIMFDAGSGTGRHIVYTFVQKVPQQLPILEGEVDSVKRGLSAFVDQKQGAETVQGL 107
 DB 44 YAVVFDAGSGTGRHIVYTFVQKVPQQLPILEGEVDSVKRGLSAFVDQKQGAETVQGL 102
 QY 108 LEVAKDSIPRSHWKTTPVVKATAGLLPEHAKALLFEVKEIFRKSPELVPKGSYIMD 166
 DB 103 LEQAEVDVDDLPQKTPVRLGATAGLLPEHAKALLFEVKEIFRKSPELVPKGSYIMD 162
 QY 167 MDGSGEGLAWTVNVLFGQLHGRQETVGLDGGASTQITFLPQFEKTLQTPRGYLTSP 222
 DB 163 IDGTQEGSVLWTVNVLFGQLHGRQETVGLDGGASTQITFLPQFEKTLQTPRGYLTSP 221
 QY 223 --GYLTSEFMENSTYKLYTHSYLGLKAAKRLATLGALETGTDGHTFRS--ACLPRLWE 278
 DB 222 DDPIYIKVVLKGIPIYDLYVHSHFGREASRAELKL-----TPRSPNPLLACFN 272
 QY 279 AEWIFGVKYOYGGNQEGBVG-FEPYAEVLVVRGKLHQPVEVQSGFYAFSYYYDRAVDMDIYDK 326
 DB 273 GIYTSGEFPKATATSG--ANPKCNVIRKAL--KLNYPCYQCTGGIWNWGGGNGQ 329
 QY 327 ---YAFSYYYDRAVDMDIYDKGG--ILKVEDFERKAREVCD-NLENTSGSPFL----- 376
 DB 330 KNLFPASSSFFVLPEDTGMVDASTPNFILRPVDIETKAEACALNEDAKSYFFLDKKNV 389
 QY 377 ----CMDLSYITALLKDGFGFADSTVLQTKVYN----IETGALGATPHLLQSL 424
 DB 390 ASYVCMDLTYQYVLLVDGFLDPLQKITSKEIEYQDAIVEAAWPLGNVAEISAL 445

RESULT 7

ID GDA1_YEAST
 AC P32621;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Guanosine-diphosphatase (EC 3.6.1.42) (GDPase).

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DR EMBL; U58597; AB02720.1; -;
 DR PIR; JC4616; JC4616;
 DR InterPro; IPR000407; GDA1_CD39_NTPase;
 DR Pfam; PF01150; GDA1_CD39; 1;
 DR PROSITE; PS01238; GDA1_CD39_NTPase; 1;
 DR PROSITE; PS01238; GDA1_CD39_NTPase; 1;
 KW Hypothetical protein; Transmembrane; Hydrolase.
 FT TRANSMEM 439 459 POTENTIAL.
 FT SEQUENCE 454 AA; 50041 MW; 905FE431DA2F52F CRC64;

Query Match 19.8%; Score 446.5; DB 1; Length 454;
 Best Local Similarity 28.8%; Pred. No. 2.6e-28;
 Matches 131; Conservative 78; Mismatches 177; Indels 69; Gaps 16;

QY 25 NQQTWFEGIFLS-----SMCPINVGA-----STLYGINEDAGSTGTRHYV 65
 DB 3 NQNHPTIILAIISVLPLSLSKNVAQPLRLHLLSHSEHYAVIFDAGSGSRVVF 62
 QY 66 TFVQKMPQQLPILEG-EVFSVKPGLSAFVDQPKQGAETVQGLLEVAKDISIPRSHWKT 124
 DB 63 RFDEKL-GLLPIGNNIEYFATEPGLSSYAEDPKAAANSLEPLLDGAGVVPQELQSETP 121
 QY 125 VVLKATAGRLRLPEHKAKALLFEVKEIFR-KSPFLVEKGSVIMDSDEGLIAWTVNEL 183
 DB 122 LELGATAGRLMLKGDAAEKILQAVNLVKNQSTFHSKDQWVITLDGTQEGSYNMAAINYL 181
 QY 184 TGLQHLGHQETVGLDGGASTQTTFE---PQPEKTLB-QTPRGYLTSPFEMENSTVKLYT 239
 DB 182 LQNLGKYKSTAIIDLGSSVQVAYALSNEQFAKQFQEDGEPYVQOKHLSKDYNLVY 241
 QY 240 HSYLGFLGKARLATLGALETGDTGHTFRSACLPFLWLEWTFPGKYVQGNQGEVG 299
 DB 242 HSYLNYGQLAGRAIFKASRNES-----NPCALEGCDGYSYGVYKVPKPKGS-- 292
 QY 300 FEPCEVAVLVVRG-KLHQPEEYQSGF-----YAPSYVYDRAVDMDI 342
 DB 293 ---SWKRCRTRHALKINAKNIEBCTFNGWNGGQKQKNIHASFYDICAQVGI 349
 QY 343 DYE-KGGILKVEDFERKAREVCD-NLENFTS-----GSPFICMDSYITALLKDGFG 392
 DB 350 DTKFPSALAKETIQLNAAKACQTNVADIKSIFPKTQDRNIPVLCMDLIYEYTLVDGFG 409
 QY 393 F---ADSTVLQLTQKVN-NIETGVALGATPHLQS 423
 DB 410 LNPHEITVIHDVQYKNYLVGAAMPGLGCAIDLVS 444

RESULT 9
 YV4E CAEEL
 ID YV4E CAEEL STANDARD; PRT; 485 AA.
 AC Q1841.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 54.3 kDa protein C33H5.14 in chromosome IV.
 GN C33H5.14.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Bradshaw H., Stellyes L.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
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 CC -----

DR EMBL; U41007; AA82272.1; -;
 DR PIR; T34147; T34147;
 DR WormPep; C33H5.14; CE04157.
 DR InterPro; IPR000407; GDA1_CD39_NTPase.
 DR Pfam; PF01150; GDA1_CD39; 1;
 DR PROSITE; PS01238; GDA1_CD39_NTPase; 1;
 DR PROSITE; PS01238; GDA1_CD39_NTPase; 1;
 KW Hypothetical protein; Transmembrane; Hydrolase.
 FT TRANSMEM 439 459 POTENTIAL.
 FT SEQUENCE 485 AA; 54309 MW; D564D1ADC20F581E CRC64;

Query Match 17.2%; Score 387.5; DB 1; Length 485;
 Best Local Similarity 27.7%; Pred. No. 1.6e-23;
 Matches 120; Conservative 84; Mismatches 152; Indels 77; Gaps 18;

QY 49 YGIMFDAGSTGTRTHVTFVQKMPQQLPILEGVFD-----VKPGLSAFVDQPKQGA 102
 DB 25 YGICVDAGSGSTRLEFVYT-LKPLSGGLTNDITLHSESEPVVKKVTPGLSFGDKPEQWE 83
 QY 103 TVQGLLEVAKDISIPRSHWKTTPVVLKATAGRLRLPEHKAKALLFEVKEIFRSPFL-VPK 161
 DB 84 YLTPLLRPAEHIPEYQGLGETDLIFATAGNRLLEPAQKDAIKNLQNGLSVTALEVSD 143
 QY 162 GSVSIMDGSDEGILAWTVNLFQLGHRQETVGLDGGASTQTTFEPEK----- 215
 DB 144 SNIRIIDGAWEGISWIAVNVILGRFDKENDSKYGMIDMGASVQIAFEIANEKESYNGG 203
 QY 216 TLEQTPRGYLTSPFEMENSTVKLYTHSYLGFLGKARLATLGALETGDTGHTFRSACLP 275
 DB 204 NYEINLGSITFEDYK--YKIYSTTFLGYNAGELKKYENSUVKSGNS-----NDSCSP 257
 QY 276 WLEAEWIFGGYVQVNGQEGEVGFPCYAEVLVVRGKLGHPF----- 319
 DB 258 GLNR---LLIG---EFTVNGTGE--WDVCLAQVSSLI-GDKAQPSCPNPTCFLRNVIA 308
 QY 320 EVQSGSFVAFS-YVDRAVDTMDIDYEGKILKVEDFERKAREVC-----ONLENFTSGSP 374
 DB 309 NLSTVQLYGFSEYWTTS-----NFGSGSEYHYQKFTDEVRKYCQKMDNDIQDGFKRNE 362
 QY 375 F-----LMDLSYITALLKDGFGFADST--VLQLTKKNNIETGVALGA----- 416
 DB 363 FENADIERLGTNCFCNAWVTSVLHDGFN-VDKTKHLFQSVLKIAGEEWMALGAWLYHSK 421
 QY 417 --TFHLLOSIGIS 427
 DB 422 DLKFNLLQLEVA 434

RESULT 10
 YBU4 CAEEL
 ID YBU4 CAEEL STANDARD; PRT; 552 AA.
 AC Q21815;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein R07E4.4 in chromosome X.
 GN R07E4.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;

RA Miller N.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBSJ databases.
 RN [2]
 RP REVISIONS.
 RA Waterston R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBSJ databases.
 CC -!- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
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 CC
 CC EMBL: U39652; AAA80403.2; -
 CC WormPep; R07E4.4; CE28748.
 CC InterPro; IPR000407; GDA1_CD39_NTPase.
 CC Pfam; PF01150; GDA1_CD39; 1.
 CC PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
 CC Hypothetical protein; Transmembrane; Hydrolase.
 FT TRANSMEM 7 27 POTENTIAL.
 FT TRANSMEM 490 510 MW; E5DC32C858AE4D94 CRC64;
 SQ SEQUENCE 552 AA; 62510 MW; E5DC32C858AE4D94 CRC64;
 Query Match 17.1%; Score 385; DB 1; Length 552;
 Best Local Similarity 28.6%; Pred. No. 3e-23;
 Matches 126; Conservative 69; Mismatches 160; Indels 86; Gaps 20;
 QY 49 YGIMPDAGSTGTRIHVYTVQVMPGQLPILGEVFDG-----VKPGLSAFVDOPKQAE 102
 DB 44 YGVICDAGSTGTRFLFYVNIWISDSBELIQIEPVIYDNKPVKKISPLSTGTGTPAQAAE 103
 QY 103 TVQGLEVAKDIPRSHWKKTPVLKATAGLLPEHKAKALLPEVKIIPKSPPL----- 158
 DB 104 YLRPLMELAEHPIPEKREYTFVFIFATAGMLIPDQBQAVL-----KNLRNKLKRTSMQ 160
 QY 159 VPKGSVIMDGDEGLIATVYVNLGTGLH-----GH-RQETVGLDGLGAST 205
 DB 161 VLKEHRLIEGWEGEYIYVNIWISDSBELIQIEPVIYDNKPVKKISPLSTGTGTPAQAAE 220
 QY 206 QITF-LPQFEK-----TLEQTPRGYTSFEMFNSTYKLYTHSYLGF-----GLKAAKLATLG 256
 DB 221 QIAFELPDTDSFSSINVENINLSCREDDSLFK--YKLFVTPFLGYGVNEGIRKYEHLMS 278
 QY 257 ALTEGTGDTGTRFESACLRWLEAEWIFGQVQVQGN--OEG-----E 297
 DB 279 KLKQD--NGTVIQDCNPLNHLKT-----VTLENGENFVRRTGTGWNWTCSEVKKLNPE 331
 QY 298 VGPEPCYAEVLVRVVRKGLHOPE-EVQSGFYAFSYVDRAVDMDIDYKGGILKVEDFE 356
 DB 332 SSSEVCKAABKCYFGAPAPSTPLSNIEWGFSEYVYSTHDV-----LGLGQYDAENIA 387
 QY 357 RKAREVCD-----NLENTFSGSP-----FLCWDLSYITALLKDGFGPADST--VLQ 400
 DB 388 KTKQYCSRWSTIQESKKQLYPRADEERLRTQCFKSMWTSVLHDSFS-VDRTHKFKQ 446
 QY 401 LTKVANNIETGVALG--TFHL 420
 DB 447 SVSTIAGQEVQWALGAMVYEM 467
 RESULT 11
 ID ENPI_CHKICK STANDARD; PRT; 493 AA.
 AC O93295;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
 DE (Ntpbase1) Ecto-ATP diphosphohydrolase (ATPbase) (Lymphoid cell
 DE activation antigen) (Ecto-apyrase) (CD39 antigen).

GN ENTED1 OR CD39.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21 AND 150-156.
 RC TISSUE=Oviduct;
 RX MEDLINE=98298108; PubMed=9632655;
 RA Nagy A.K., Knowles A.F., Nagami G.T.;
 RT "Molecular cloning of the chicken oviduct ecto-ATP.
 RT diphosphohydrolase.";
 RL J. Biol. Chem. 273:16043-16049 (1998).
 RN [2]
 RP SEQUENCE OF 1-17.
 RC TISSUE=Stomach;
 RX MEDLINE=97442428; PubMed=9295305;
 RA Lewis-Carl S., Kirley T.L.;
 RT "Immunolocalization of the ecto-ATPase and ecto-apyrase in chicken
 RT gizzard and stomach. Purification and N-terminal sequence of the
 RT stomach ecto-apyrase.";
 RL J. Biol. Chem. 272:23645-23652 (1997).
 CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
 CC nucleotides to regulate purinergic neurotransmission. Could also
 CC be implicated in the prevention of platelet aggregation.
 CC Hydrolyzes ATP and ADP equally well (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
 CC -!- COFACTOR: REQUIRES CALCIUM AND MAGNESIUM (BY SIMILARITY).
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- PTM: N-GLYCOSYLATED.
 CC -!- SIMILARITY: BELONGS TO THE GDA1 / CD39 NTPASE FAMILY.
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 CC
 CC EMBL: AF041355; AAC26491.1; -
 CC InterPro; IPR000407; GDA1_CD39_NTPase.
 CC Pfam; PF01150; GDA1_CD39; 1.
 CC PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
 CC Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
 FT DOMAIN 1 2 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 8 28 POTENTIAL.
 FT DOMAIN 29 463 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 464 486 POTENTIAL.
 FT DOMAIN 487 493 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 65 65 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 267 267 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 324 324 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 330 330 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 361 361 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 382 382 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 16 16 C -> W (IN REF. 2).
 FT CONFLICT 21 21 I -> G (IN REF. 1; AA SEQUENCE).
 SQ SEQUENCE 493 AA; 54034 MW; F14FF4C3AA2F3603 CRC64;
 Query Match 17.0%; Score 383; DB 1; Length 493;
 Best Local Similarity 27.3%; Pred. No. 3.7e-23;
 Matches 131; Conservative 66; Mismatches 170; Indels 112; Gaps 18;
 QY 11 MLVYSCVSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGTRIHVYTF-VQ 69

Db 11 LITATCVSIIAIIILSANDVDKDFVL-----PPGTYGLVDFDAGSTHTALYVYQWPAD 62
 QY 70 KNEGQULILEGEVDFSVKPLGSAFVDQPKQGAETVQGLLEVAKDSIPRSHWKTTPVVLKA 129
 Db 63 KENGTIVSQVESCTVWGSGISYADDPAAGASLKPCLDKAKAVIPVEQQWQTPTYLGA 122
 QY 130 TAGLRLPH-----KAKALLFEVKEIIPKSPFIVPKGSVIMDSBEGILAWVTNPLTQ 186
 Db 123 TAGMLLRQNSTKAEQVAPKAIREFP--VDFRGAQILCNBEGSGMTVNYLLET 180
 QY 187 L-----HGRQETVGLDLGGASTQITFLPQFECTLTQTPRGYLTSPFEMENSTYK 236
 Db 181 LKFSFAGKWEHPQNTVEUGALDLGGASTQITFQGV--TIEDKNTSVL--FRLYGTNVS 236
 QY 237 LYTHSYLGLKAAKRLATLGALETEGDTGHTFRSACLPRWLEAEWIFGKVKYQYGNQB- 295
 Db 237 LYTHSYLGLKAAKRLATLGALETEGDTGHTFRSACLPRWLEAEWIFGKVKYQYGNQB- 295
 QY 296 ---GEVGFEPY-----AEVLVVR----- 317
 Db 281 ITIAGIYOSPCVFTSMSPQAQILVTGTGNPAACPTAILKLFNLTGCGANRTCGFDGVYQ 340
 QY 318 PEEVORGSEYAFS-YYIDRA-----VDTMDIDY-EKGGILKVEDFERKAREVC 363
 Db 341 PP--VRGQFFAFAGFYITTSFLNLTCQSLSHVNATWDFCNKNSSELVETFPQNK---- 394
 QY 364 DNLENFTSGPFLNDLSYITALLKDGFGFADST--VLQLTAKVNNIEFGWALGATFHL 420
 Db 395 EHLTY-----CVVGLYILTLVDGKAFDEHTWSNIHFSKAGNADIGMTLGFMLNL 446

RESULT 12

YND1_YEAST STANDARD; PRT; 630 AA.
 AC P40009;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Golgi apyrase (EC 3.6.1.5) (ATP-diphosphatase) (Adenosine
 DE diphosphatase) (ADPase) (ATP-diphosphohydrolase) (Golgi nucleoside
 DE diphosphatase).
 GN YND1 OR YER005W.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=S288c;
 RX MEDLINE=99340091; PubMed=10409709;
 RA Gao X.D., Kaigorodov V., Jigami Y.,
 RT "YND1, a homologue of GDAL, encodes membrane-bound apyrase required
 RL for Golgi N- and O-glycosylation in Saccharomyces cerevisiae.";
 RL J. Biol. Chem. 274:21450-21456(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RX PubMed=9169868;
 RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
 RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
 RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
 RA Hunnicke-Smith S., Hynan R.W., Kayser A., Komp C., Lashkari D., Lew H.,
 RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
 RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
 RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
 RL Nature 387:78-81(1997).
 CC -!- FUNCTION: CATALYZES THE HYDROLYSIS OF PHOSPHOANHYDRIDE BONDS OF
 CC NUCLEOSIDE TRI- AND DI-PHOSPHATES. HAS EQUAL HIGH ACTIVITY TOWARD
 CC ADP/ATP, GDP/GTP, AND UDP/UTP AND APPROXIMATELY 50% LESS TOWARD
 CC CDP/CTP AND THIAMINE PYRIPHOSPHATE. HAS NO ACTIVITY TOWARD GMP.
 CC REQUIRED FOR GOLGI GLYCOSYLATION AND CELL WALL INTEGRITY.

CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
 CC -!- PATHWAY: Glycosylation.
 CC -!- SUBCELLULAR LOCATION: MEMBRANE BOUND; GOLGI.
 CC -!- SIMILARITY: BELONGS TO THE GDAL / CD39 NTPASE FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF203695; AAF17573.1; -;
 DR EMBL; U18778; AAB64538.1; -;
 DR PIR; S50463; S50463.
 DR SGD; S0000807; YND1.
 DR GO; GO:0006486; P:protein amino acid glycosylation; IMP.
 DR InterPro; IPR00407; GDAL_CD39_NTPase.
 DR Pfam; PF01150; GDAL_CD39; 1.
 DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
 KW Hydrolase; Transmembrane; Golgi stack.
 FT DOMAIN 1 500
 FT TRANSMEM 501 517 POTENTIAL.
 FT DOMAIN 518 630 CYTOPLASMIC (POTENTIAL).
 FT SEQUENCE 630 AA; 71851 MW; 02F8D24A78212544 CRC64;
 SQ
 Query Match 16.5%; Score 372; DB 1; Length 630;
 Best Local Similarity 26.2%; Pred. No. 3.9e-22;
 Matches 117; Conservative 73; Mismatches 165; Indels 92; Gaps 17;
 QY 49 YGIMPDAAGTGTTHVYTF-----VQMPQQLPILGE-----VFDSVKPGLSA 92
 Db 10 FGIVIDAGSGSRHVFVKMQDTESLLHATNDSQSILOSIVPHIQEKDWT- KLNPLGLSS 68
 QY 93 FVDOPKQGAET-VQGLLEVAKDSIPRSHWKTTPVVLKATAGLRLPHEKAKALLFEV-KE 150
 Db 69 PEKFPQDAYKSHIKPDLDFAKNIPESHWSSCPFIQATAGWRLLPQDIQSILGLCQG 128
 QY 151 IFRKSPFIVP--KGSVIMDSBEGILAWVTNPLTQGLHGRQF-----TVGTLDLGA 203
 Db 129 LKHPAEFLVEDCSAQIQVIDGETEGLYCWLGLNLYGHFNVDYNPEVSDHFTFGFMDMGA 188
 QY 204 STQITFLPQFEKTL-----QTPRGYLTSPFEMFNSTYKLYTHSYLGLKAAKRL 252
 Db 189 STQITAFAPHSDSGEIARHDDIATIFLRSVNGDLQKMDVFST-----WLGFGANQARR 241
 QY 253 ATLGAL-----ETEGTDGHTFRSACLPRWLEAEWIFGKVKYQYGNQGEVGF 301
 Db 242 RYLAQLINTLPENTNDYENDDFSTRLNDPCMRGSSSTDFFPKDTIFHIAGSGNYEQCTK 301
 QY 302 PCYAEVLR-----VVRGKLHQPE-EVQRGSFYAFSYYYDRAVDTMDIDYEKGILVK 352
 Db 302 SIYPLLLKNMPCDDPECLFNGVHAPRIDFANDKFIGTSEYWTANDV----FKLGGEYNF 357
 QY 353 EDFERKAREVCN-----LENFTSG-----SPFL-----CMLSVITALLKDGFGFA----- 394
 Db 358 DKFSKSLREFCNSNWTOLANSKGVYNSIPENFLKDACFKGNVNLITLHEGDFMPTDV 417
 QY 395 -----DSTVLQLTAKVNNIETGVALG 415
 Db 418 DAENVNDEPLFQSVKEKVEERLSWTLG 444
 RESULT 13
 ENP1_MOUSE
 ID ENP1_MOUSE STANDARD; PRT; 510 AA.
 AC P55772;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
 DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 13, 2003, 06:08:47 ; Search time 49 Seconds
(without alignments)
1386.428 Million cell updates/sec

Title: US-09-905-744B-6

Perfect score: 2250

Sequence: 1 MATSWGTFFMLVSVCSA.....ETGALGATFHLQSLGISH 428

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

- 1: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1980.DAT.*
- 2: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1981.DAT.*
- 3: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1982.DAT.*
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- 8: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1987.DAT.*
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- 12: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1991.DAT.*
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- 18: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1997.DAT.*
- 19: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1998.DAT.*
- 20: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1999.DAT.*
- 21: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2001.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2250	100.0	428	21	Human CD39-L4 prot
2	2250	100.0	428	22	Human CD39 like pr
3	2250	100.0	428	22	Human CD39 like pr
4	2250	100.0	428	21	Human CD39-L4 prote
5	2235	99.3	428	21	Human CD39-L4 vari
6	2235	99.3	428	22	Human CD39 like pr
7	2104	93.5	405	21	Human CD39-L66 pro
8	2104	93.5	405	22	Human CD39 like pr
9	1832.5	81.4	465	23	Mouse CD39L4 prote

10	1660	73.8	330	21	AA533336	Human colon cancer
11	999	44.4	456	23	AAE19881	Human CD39L2 prote
12	999	44.4	484	22	AAE19881	Human CD39 like pr
13	996	44.3	463	23	AB06124	Human NS protein s
14	996	44.3	467	23	AB06124	Human NS protein s
15	992	44.1	456	22	AB06124	Human NS protein s
16	989	44.0	446	23	AB06124	Human NS protein s
17	897	39.9	462	22	AAU0882	Human polypeptide,
18	819.5	36.4	471	22	AAU0882	Novel human secret
19	696.5	31.0	461	22	AB062243	Novel human CD39
20	696.5	31.0	464	22	AB062243	Novel human CD39
21	590	26.2	476	21	AAU0882	Drosophila melanog
22	590	26.2	476	21	AAU0882	Drosophila melanog
23	533	23.7	476	21	AAU0882	Human CD39-L4-2/3
24	533	23.7	476	21	AAU0882	Human CD39-L4-2/3
25	507.5	22.6	486	20	AAU0882	Human CD39-L4-1 pr
26	507.5	22.6	486	20	AAU0882	Human CD39-L4-1 pr
27	499.5	22.2	467	20	AAU0882	Human CD39-L4-1 pr
28	498	22.1	462	20	AAU0882	Human CD39-L4-1 pr
29	498	22.1	462	20	AAU0882	Human CD39-L4-1 pr
30	491.5	21.8	496	23	AAU0882	Human CD39-L4-1 pr
31	489	21.7	455	22	AAU0882	Human CD39-L4-1 pr
32	488	21.7	472	24	AB06124	Human CD39-L4-1 pr
33	482.5	21.4	496	20	AAU0882	Human CD39-L4-1 pr
34	367	16.3	495	20	AAU0882	Human CD39-L4-1 pr
35	358.5	15.9	458	22	AAU0882	Human CD39-L4-1 pr
36	358.5	15.9	458	22	AAU0882	Human CD39-L4-1 pr
37	358.5	15.9	458	24	AB06124	Human CD39-L4-1 pr
38	358.5	15.9	458	24	AB06124	Human CD39-L4-1 pr
39	358.5	15.9	458	24	AB06124	Human CD39-L4-1 pr
40	358.5	15.9	458	24	AB06124	Human CD39-L4-1 pr
41	358.5	15.9	458	24	AB06124	Human CD39-L4-1 pr
42	358.5	15.9	458	24	AB06124	Human CD39-L4-1 pr
43	358.5	15.9	458	24	AB06124	Human CD39-L4-1 pr
44	358.5	15.9	458	24	AB06124	Human CD39-L4-1 pr
45	354.5	15.8	474	21	AAU0882	Human CD39-L4-1 pr

ALIGNMENTS

RESULT 1

AAU4849
ID AAU4849 standard; Protein; 428 AA.

XX AAU4849;

XX AC

XX 18-MAY-2000 (first entry)

XX DT

XX DE Human CD39-L4 protein.

XX XX

XX CD39-L4; human; apyrase; nucleotide diphosphatase; NDPase;

XX KW ATP diphosphohydrolase; ATPase; adenosine diphosphate; ADP; treatment;

XX KW platelet aggregation; antithrombotic; thrombosis; myocardial infarction;

XX KW cerebral ischaemia; angina; vascular graft; extracorporeal circulation;

XX KW molecular weight marker; nutritional supplement; tumour; prevention;

XX KW drug targeting; Apyrase Conserved Region; ACR.

XX OS Homo sapiens.

XX XX

XX Key

XX Peptide

XX Location/Qualifiers

XX 1..22

XX /label= Leader_peptide

XX 23..428

XX /label= Mature_human_CD39-L4_protein

XX /note= "Homologous to human and murine CD39"

XX Binding-site

XX 54..58

XX /label= ATP_Binding_region

XX 129..134

XX /label= Apyrase_Conserved_Region

XX 169..173

XX /label= Apyrase_Conserved_Region

XX 199..206


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XX  Sequence 428 AA;
SQ
Query Match 100.0%; Score 2250; DB 22; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.9e-208;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSWGTVFVFMVSVCSAVSHRNQQTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVFVFMVSVCSAVSHRNQQTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTVPVLKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180
DB 121 KKTVPVLKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180
QY 181 NFLTQGLHGRHROETVGTDLGGASTQITFLPOFEKTLQTPRGYLTSPFENSTYKLYTH 240
DB 181 NFLTQGLHGRHROETVGTDLGGASTQITFLPOFEKTLQTPRGYLTSPFENSTYKLYTH 240
QY 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGVKYQVGGNQEVEGF 300
DB 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGVKYQVGGNQEVEGF 300
QY 301 EPCYAEVLVRVGRKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTQKVNNIETGVALGATFHL 420
DB 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTQKVNNIETGVALGATFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 3
AAB72243
ID AAB72243 standard; Protein; 428 AA.
XX
AC AAB72243;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human CD39 like protein CD39-L4 amino acid sequence.
XX
KW Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
KW cerebral artery thrombosis; platelet aggregation; inflammation;
KW apoptosis; autoimmune disorder; neurological disorder;
KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.
XX
OS Homo sapiens.
XX
FN WO200110205-A1.
XX
PD 15-FEB-2001.
XX
PF 09-AUG-2000; 2000WO-US21790.
XX
PR 01-AUG-1999; 98US-0370265.
PR 11-JAN-2000; 2000US-0481238.
PR 25-APR-2000; 2000US-0557800.
PR 30-JUN-2000; 2000US-0583231.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ford J, Mulero JJ, Yeung G;

```

```

XX  Sequence 428 AA;
DR N-PSDB; AAF63402.
XX
PT Polynucleotides encoding human CD39-like polypeptides, with apyrase
PT and/or NDPase activity, which are useful in the treatment of
PT pathological conditions caused by thrombosis (e.g. myocardial
PT infarction) and inflammatory disorders.
XX
PS Example 9; Page 142-144; 203pp; English.
XX
CC This invention relates to polynucleotides encoding human CD39-like
CC polypeptides with apyrase and/or NDPase activity. The polypeptides having
CC ATPase, including NDPase, activity are useful for inhibiting platelet
CC function and can therefore be used in the prophylaxis or treatment of
CC pathological conditions caused by or involving thrombosis or excessive
CC coagulation or excessive platelet aggregation, such as myocardial
CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
CC artery thrombosis or intracardiac thrombosis, and conditions associated
CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
CC modulating disease states (including platelet aggregation, inflammation
CC and apoptosis) associated with ADP or other purinergic signalling by
CC reducing the levels of NDPs. The polypeptides are also useful for
CC prophylaxis or treatment of inflammation related disorders, such as
CC disorders involving sepsis or systemic inflammatory response syndrome or
CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
CC cytokine overstimulation); autoimmune disorders such as thrombosis,
CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
CC neurological disorders including neurodegenerative diseases, epilepsy,
CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, and amyotrophic lateral sclerosis; and cancer. The present
CC sequence represents the CD39 like protein CD39-L4 amino acid sequence.
XX
SQ Sequence 428 AA;

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Query Match 100.0%; Score 2250; DB 22; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.9e-208;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MATSWGTVFVFMVSVCSAVSHRNQQTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVFVFMVSVCSAVSHRNQQTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTVPVLKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180
DB 121 KKTVPVLKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180
QY 181 NFLTQGLHGRHROETVGTDLGGASTQITFLPOFEKTLQTPRGYLTSPFENSTYKLYTH 240
DB 181 NFLTQGLHGRHROETVGTDLGGASTQITFLPOFEKTLQTPRGYLTSPFENSTYKLYTH 240
QY 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGVKYQVGGNQEVEGF 300
DB 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGVKYQVGGNQEVEGF 300
QY 301 EPCYAEVLVRVGRKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTQKVNNIETGVALGATFHL 420
DB 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTQKVNNIETGVALGATFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

```

RESULT 4
AAE19883
ID AAE19883 standard; Protein; 428 AA.
XX
AC AAE19883;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human CD39L4 protein.
XX
KW Human; CD-39-like protein; CD39L4 protein; therapy; immune deficiency;
KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; aschma;
KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
KW osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer;
KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
KW nervous system disease; nerve injury; ischaemia-reperfusion injury;
KW endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
KW Crohn's disease; virucide; antibacterial; antifungal; neuroprotective;
KW dermatological; immunosuppressive; vulnary; nootropic; anticonvulsant;
KW antiinflammatory; nephrotropic; gastrointestinal; vasotropic.
XX
OS Homo sapiens.
XX
FN US6350447-B1.
XX
PD 26-FEB-2002.
XX
PF 29-JAN-1999; 99US-0240639.
XX
PR 29-JAN-1999; 99US-0240639.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Chadwick BP, Frischauf A;
XX
DR WPI; 2002-215262/27.
DR N-PSDB; AAD31695.
XX
PT An isolated polypeptide with phosphohydrolase activity, designated
PT CD39L2, useful to identify other proteins with which binding occurs or
PT identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
PT sclerosis and osteoporosis -
XX
PS Example; Fig 7; 101bp; English.
XX
CC The present invention relates to novel proteins with phosphohydrolase
CC activity, designated CD-39-like (CD39L) proteins and polynucleotides
CC encoding such proteins. CD39L proteins are useful to treat infectious
CC diseases caused by viral, bacterial, fungal or other infection that may
CC be treatable with CD39L. They are useful in the treatment of various
CC immune deficiencies and disorders, autoimmune disorders such as multiple
CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
CC thyroiditis and insulin dependent diabetes mellitus, allergic reactions
CC and conditions such as asthma and other respiratory problems, periodontal
CC disease, osteoporosis, osteoarthritis and other tooth repair processes.
CC They may have utility in compositions used for bone, cartilage, tendon,
CC ligament and/or nerve tissue growth or regeneration as well as for wound
CC healing and tissue repair and replacement and in the treatment of burns,
CC incisions and ulcers. CD39L proteins may also be useful for proliferation
CC of neural cells and for regeneration of nerve and brain tissue, i.e. for
CC the treatment of central nervous system diseases such as Alzheimer's
CC disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
CC disease, peripheral nervous system diseases peripheral nerve injuries,
CC peripheral neuropathy and localised neuropathies. They are also used to
CC treat mechanical and traumatic disorders which involve degeneration of,
CC death or trauma to neural cells or nerve tissue. CD39L proteins of the
CC invention are also useful to promote better or faster closure of non-
CC healing wounds, including pressure ulcers, ulcers associated with
CC vascular insufficiency and surgical and traumatic wounds. They also
CC exhibit anti-inflammatory activity and may be used to treat inflammatory
CC conditions including chronic or acute conditions, including ischaemia-
CC reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine

CC or chemokine-induced lung injury, inflammatory bowel disease or Crohn's
CC disease. The present sequence is human CD39L4 protein.
XX
SQ Sequence 428 AA;
Query Match 100.0%; Score 2250; DB 23; Length 428;
Best Local Similarity 100.0%; Pred. NO. 2.9e-208;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATSWGTVPFVLMVSCVSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVPFVLMVSCVSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHYVTFVQKMPGQLPILEGVEFDSVKPGLSAFVDQPKQGAETVQGLLEVAKOSIPRSHW 120
DB 61 RIHYVTFVQKMPGQLPILEGVEFDSVKPGLSAFVDQPKQGAETVQGLLEVAKOSIPRSHW 120
QY 121 KKTVPVLKATAGLLPEHAKALLPEVKIIFRKSPLVPKGSVIMDSGDEGILAWTV 180
DB 121 KKTVPVLKATAGLLPEHAKALLPEVKIIFRKSPLVPKGSVIMDSGDEGILAWTV 180
QY 181 NFLTQQLHGHQETVGTLDLGGASTQITFLPQPEKTEQTPRGYLTSEFMENSTYKLYTH 240
DB 181 NFLTQQLHGHQETVGTLDLGGASTQITFLPQPEKTEQTPRGYLTSEFMENSTYKLYTH 240
QY 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVYQYGGNQEVEGVP 300
DB 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVYQYGGNQEVEGVP 300
QY 301 EPCYAEVLVRVGRKLHQPVEEVQVGSFYAFSYYYDRAVDTDMDIYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKLHQPVEEVQVGSFYAFSYYYDRAVDTDMDIYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCHDLSYITALLKDGFGFADSTVLOLTKKVNNIETGALGATFHL 420
DB 361 EVCNLENFTSGSPFLCHDLSYITALLKDGFGFADSTVLOLTKKVNNIETGALGATFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428
RESULT 5
AAE19883
ID AAY44850 standard; Protein; 428 AA.
XX
AC AAY44850;
XX
DT 18-MAY-2000 (first entry)
XX
DE Human CD39-L4 variant-ACR III mutant protein.
XX
KW CD39-L4; human; apyrase; nucleotide diphosphatase; NDPase; variant;
KW ATP diphosphohydrolase; ATPDase; adenosine diphosphate; ADP; treatment;
KW platelet aggregation; antithrombotic; thrombosis; myocardial infarction;
KW cerebral ischaemia; angina; vascular graft; extracorporeal circulation;
KW molecular weight marker; nutritional supplement; tumour; prevention;
KW drug targeting; substitution mutation.
XX
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 168 /note= "Wild type Asp substituted with Thr"
FT Misc-difference 170 /note= "Wild type Ser substituted with Gln"
FT Misc-difference 175 /note= "Wild type Leu substituted with Phe"
XX
PN WO200004041-A2.
XX
PD 27-JAN-2000.

XX PF 16-JUL-1999; 99WO-US16180.
 XX PR 16-JUL-1998; 98US-0118205.
 XX PR 24-JUL-1998; 98US-0122449.
 XX PR 04-FEB-1999; 98US-0244444.
 XX PR 19-MAR-1999; 98US-0273447.
 XX PR 09-JUL-1999; 99US-0350836.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Ford J, Mulero JJ;
 XX PR WPI; 2000-182397/16.
 DR N-PSDB; AA250357.
 XX PR New nucleic acid encoding human CD39-like protein, useful for treating
 PT and preventing thrombotic disease -
 XX PS Claim 17; Fig 6; 125pp; English.
 CC The present amino acid sequence is the CD39-L4 variant, designated
 CC as ACR III mutant protein, an apyrase and/or nucleotide diphosphatase
 CC (NDPase). It is isolated from the human foetal liver-spleen cDNA library,
 CC b2HFLS20W. It is a soluble ATP Diphosphohydrolases (ATPDase) and is
 CC involved in the hydrolysis of adenosine diphosphate (ADP), the agonist
 CC that causes platelet aggregation. CD39-L4 protein has 30% and 80%
 CC homology to human and murine CD39. It has platelet aggregation inhibition
 CC and antithrombotic activity. CD39-L4 is used to treat or prevent
 CC thrombosis, myocardial infarction, cerebral ischaemia and angina. It is
 CC also used in vitro, to maintain vascular grafts or during extracorporeal
 CC circulation, to hydrolyse NDP, as molecular weight markers and as
 CC nutritional supplements. It is used to identify therapeutic agents that
 CC bind and modulate CD39-L4. It is coupled to toxins for targeting drugs
 CC to tumours or other cells that express CD39-L4.
 XX SQ Sequence 428 AA;
 Query Match 99.3%; Score 2235; DB 21; Length 428;
 Best Local Similarity 99.3%; Pred. No. 8.1e-207;
 Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MATSGTFFMLVSCVCSAVSHRNQQTWFGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSGTFFMLVSCVCSAVSHRNQQTWFGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 QY 61 RIHVYTFVQKMPGQLPILEGVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHVYTFVQKMPGQLPILEGVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 QY 121 KKTTPVLKATAGRLPEHKAKALLPEVKEIFRKSPLVPKGSVIMDGSDEGILAVTV 180
 DB 121 KKTTPVLKATAGRLPEHKAKALLPEVKEIFRKSPLVPKGSVIMDGSDEGILAVTV 180
 QY 181 NFLTQGLHGRQETVGTLDLGASTQITFLPQFEXTLEQTPRGVLTSEMFNSTVLYTH 240
 DB 181 NFLTQGLHGRQETVGTLDLGASTQITFLPQFEXTLEQTPRGVLTSEMFNSTVLYTH 240
 QY 241 SYLGFGLKAARLATLGALETGDTGHTPRACLPRLWLAEMIFGVKYQYGGNQEVEGVF 300
 DB 241 SYLGFGLKAARLATLGALETGDTGHTPRACLPRLWLAEMIFGVKYQYGGNQEVEGVF 300
 QY 301 EPCVAELVRVRGKLHQPVEVQSGSFYAFSYVDRAVDTMDIDYKGGILKVEDPERKAR 360
 DB 301 EPCVAELVRVRGKLHQPVEVQSGSFYAFSYVDRAVDTMDIDYKGGILKVEDPERKAR 360
 QY 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNINETGWLCAIFHL 420
 DB 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNINETGWLCAIFHL 420
 QY 421 LQSLGISH 428
 DB 421 LQSLGISH 428

RESULT 6
 AAB72240
 ID AAB72240 standard; Protein; 428 AA.
 XX AAB72240;
 AC AAB72240;
 XX 14-MAY-2001 (first entry)
 DT Human CD39 like protein CD39-L4 variant ACRIII amino acid sequence.
 DE Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
 KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
 KW cerebral artery thrombosis; platelet aggregation; inflammation;
 KW apoptosis; autoimmune disorder; neurological disorder; mutant; murein;
 KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.
 XX Homo sapiens.
 OS WO200110205-A1.
 PN 15-FEB-2001.
 PD 09-AUG-2000; 2000WO-US21790.
 PF 09-AUG-1999; 99US-0370265.
 PR 11-JAN-2000; 2000US-0481238.
 PR 25-APR-2000; 2000US-0557800.
 PR 26-MAY-2000; 2000US-0583231.
 PR 30-JUN-2000; 2000US-0608285.
 XX (HYSE-) HYSEQ INC.
 FA Ford J, Mulero JJ, Yeung G;
 XX WPI; 2001-147489/15.
 DR N-PSDB; AAF63385.

Polynucleotides encoding human CD39-like polypeptides, with apyrase
 and/or NDPase activity, which are useful in the treatment of
 pathological conditions caused by thrombosis (e.g. myocardial
 infarction) and inflammatory disorders -

Claim 19; Fig 6; 203pp; English.

This invention relates to polynucleotides encoding human CD39-like
 polypeptides with apyrase and/or NDPase activity. The polypeptides having
 ATPase, including NDPase, activity are useful for inhibiting platelet
 function and can therefore be used in the prophylaxis or treatment of
 pathological conditions caused by or involving thrombosis or excessive
 coagulation or excessive platelet aggregation, such as myocardial
 infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
 artery thrombosis or intracardiac thrombosis, and conditions associated
 with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
 modulating disease states (including platelet aggregation, inflammation
 and apoptosis) associated with ADP or other purinergic signalling by
 reducing the levels of NDPs. The polypeptides are also useful for
 prophylaxis or treatment of inflammation related disorders, such as
 disorders involving sepsis or systemic inflammatory response syndrome or
 SIRS (and associated conditions such as fever, tachycardia, tachypnea,
 cytokine overstimulation; autoimmune disorders such as thrombosis,
 atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
 cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
 neurological disorders including neurodegenerative diseases, epilepsy,
 depression, Alzheimer's disease, Parkinson's disease, Huntington's
 disease, and amyotrophic lateral sclerosis; and cancer. The present
 sequence represents human CD39 like protein CD39-L4 variant ACRIII.

SQ Sequence 428 AA;

Query Match 99.3%; Score 2235; DB 22; Length 428;
 Best Local Similarity 99.3%; Pred. No. 8.1e-207;

Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATSWGTFFMLVVCVCSAVSHRNQOTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSWGTFFMLVVCVCSAVSHRNQOTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHYVTVFQKMPQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHYVTVFQKMPQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

QY 121 KKTVPVLKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180
 DB 121 KKTVPVLKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180

QY 181 NELTGQHGHRQETVGTDLGGASTOITFLPOFEKTLQTPRGYLTSPFEMNSTYKLYTH 240
 DB 181 NELTGQHGHRQETVGTDLGGASTOITFLPOFEKTLQTPRGYLTSPFEMNSTYKLYTH 240

QY 241 SYLGFGLKAARLATLGALETGDTGHTFRSACLPRWLEAEWIFGVKYQYGGNQEVEVF 300
 DB 241 SYLGFGLKAARLATLGALETGDTGHTFRSACLPRWLEAEWIFGVKYQYGGNQEVEVF 300

QY 301 EPCYAEVLVRVGRKHLQHPVEVQSGSFYAFSYYYDRAVDTMDIYKGGILKVEDFERKAR 360
 DB 301 EPCYAEVLVRVGRKHLQHPVEVQSGSFYAFSYYYDRAVDTMDIYKGGILKVEDFERKAR 360

QY 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGVALGATPHL 420
 DB 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGVALGATPHL 420

QY 421 LQSLGISH 428
 DB 421 LQSLGISH 428

RESULT 7
 AAY44851
 ID AAY44851 standard; Protein; 405 AA.

XX AC AAY44851;
 XX DT 18-MAY-2000 (first entry)
 XX DE Human CD39-L66 protein.

XX KW CD39-L66; human; CD39-L66; apyrase; nucleotide diphosphatase; NDPase;
 KW ATP diphosphohydrolyase; ATPase; adenosine diphosphate; ADP; treatment;
 KW platelet aggregation; antithrombotic; thrombosis; myocardial infarction;
 KW cerebral ischaemia; angina; vascular graft; extracorporeal circulation;
 KW molecular weight marker; nutritional supplement; tumour; prevention;
 KW drug targeting; splice variant.

XX OS Homo sapiens.
 XX PN WO200004041-A2.
 XX PD 27-JAN-2000.

XX PF 16-JUL-1999; 99WO-US16180.
 XX PR 16-JUL-1998; 98US-0118205.
 XX PR 24-JUL-1998; 98US-0122449.
 XX PR 04-FEB-1999; 99US-0244444.
 XX PR 19-MAR-1999; 99US-0273447.
 XX PR 09-JUL-1999; 99US-0350836.

XX PA (HYSB-) HYSEQ INC.
 XX PI Ford J, Mulero J;
 XX DR WPI; 2000-182397/16.
 XX DR 'N-PSDB; AA250358.

PT New nucleic acid encoding human CD39-L66 protein, useful for treating
 and preventing thrombotic disease -
 XX Claim 15; Page 124-125; 125pp; English.

CC The present amino acid sequence is the CD39-L66 protein, a splice
 variant of the CD39-L4 protein. It is an apyrase and/or nucleotide
 diphosphatase (NDPase), isolated from the human foetal liver-spleen cDNA
 library, B2HFUS20W. It is a soluble ATP diphosphohydrolase (ATPDase) and
 is involved in the hydrolysis of adenosine diphosphate (ADP), the agonist
 that causes platelet aggregation. CD39-L4 protein has 30% and 80%
 homology to human and murine CD39. It has platelet aggregation inhibition
 and antithrombotic activity. CD39-L4 is used to treat or prevent
 thrombosis, myocardial infarction, cerebral ischaemia and angina. It is
 also used in vitro, to maintain vascular grafts or during extracorporeal
 circulation, to hydrolyse NDP, as molecular weight markers and as
 nutritional supplements. It is used to identify therapeutic agents that
 bind and modulate CD39-L4. It is coupled to toxins for targeting drugs
 to tumours or other cells that express CD39-L4.

XX Sequence 405 AA;

Query Match 93.5%; Score 2104; DB 21; Length 405;
 Best Local Similarity 100.0%; Pred. No. 3.3e-194;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSWGTFFMLVVCVCSAVSHRNQOTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSWGTFFMLVVCVCSAVSHRNQOTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHYVTVFQKMPQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHYVTVFQKMPQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

QY 121 KKTVPVLKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180
 DB 121 KKTVPVLKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMDGSDEGILAWTV 180

QY 181 NELTGQHGHRQETVGTDLGGASTOITFLPOFEKTLQTPRGYLTSPFEMNSTYKLYTH 240
 DB 181 NELTGQHGHRQETVGTDLGGASTOITFLPOFEKTLQTPRGYLTSPFEMNSTYKLYTH 240

QY 241 SYLGFGLKAARLATLGALETGDTGHTFRSACLPRWLEAEWIFGVKYQYGGNQEVEVF 300
 DB 241 SYLGFGLKAARLATLGALETGDTGHTFRSACLPRWLEAEWIFGVKYQYGGNQEVEVF 300

QY 301 EPCYAEVLVRVGRKHLQHPVEVQSGSFYAFSYYYDRAVDTMDIYKGGILKVEDFERKAR 360
 DB 301 EPCYAEVLVRVGRKHLQHPVEVQSGSFYAFSYYYDRAVDTMDIYKGGILKVEDFERKAR 360

QY 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQ 400
 DB 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQ 400

RESULT 8
 AAB72239
 ID AAB72239 standard; Protein; 405 AA.

XX AC AAB72239;
 XX DT 14-MAY-2001 (first entry)
 XX DE Human CD39 like protein CD39-L4 amino acid sequence.

XX KW Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
 KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
 KW cerebral artery thrombosis; platelet aggregation; inflammation;
 KW apoptosis; autoimmune disorder; neurological disorder;
 KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.
 XX OS Homo sapiens.

EN WO200110205-A1.
 XX 15-FEB-2001.
 XX 09-AUG-2000; 2000WO-US21790.
 XX 09-AUG-1999; 98US-0370265.
 XX 11-JAN-2000; 2000US-0481238.
 XX 25-MAY-2000; 2000US-0557800.
 XX 26-APR-2000; 2000US-0583231.
 XX 30-JUN-2000; 2000US-0608285.
 XX (HYSE-) HYSEQ INC.
 XX Ford J, Mulero JJ, Yeung G;
 XX WPI; 2001-147489/15.
 XX N-PSDB; AAF63384.
 XX Polynucleotides encoding human CD39-like polypeptides, with apyrase
 PT and/or NDFase activity, which are useful in the treatment of
 PT pathological conditions caused by thrombosis (e.g. myocardial
 PT infarction) and inflammatory disorders -
 XX Claim 17; Page 157-158; 203pp; English.
 XX This invention relates to polynucleotides encoding human CD39-like
 CC polypeptides with apyrase and/or NDFase activity. The polypeptides having
 CC ATPase, including NDFase, activity are useful for inhibiting platelet
 CC function and can therefore be used in the prophylaxis or treatment of
 CC pathological conditions caused by or involving thrombosis or excessive
 CC coagulation or excessive platelet aggregation, such as myocardial
 CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
 CC artery thrombosis or intracardiac thrombosis, and conditions associated
 CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
 CC modulating disease states (including platelet aggregation, inflammation
 CC and apoptosis) associated with ADP or other purinergic signalling by
 CC reducing the levels of NDFase. The polypeptides are also useful for
 CC prophylaxis or treatment of inflammation related disorders, such as
 CC disorders involving sepsis or systemic inflammatory response syndrome or
 CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
 CC cytokine overstimulation); autoimmune disorders such as thrombosis,
 CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
 CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
 CC neurological disorders including neurodegenerative diseases, epilepsy,
 CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
 CC disease, and amyotrophic lateral sclerosis; and cancer. The present
 CC sequence represents human CD39 like protein CD39-L4.
 XX Sequence 405 AA;
 SQ
 Query Match 93.5%; Score 2104; DB 22; Length 405;
 Best Local Similarity 100.0%; Pred. No. 3.3e-194;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATSWGTVFVFLVSVCSVASHRNQQTWPEGIFLSSMCPINVSASTLYGIMFDAGSTG 60
 DB 1 MATSWGTVFVFLVSVCSVASHRNQQTWPEGIFLSSMCPINVSASTLYGIMFDAGSTG 60
 QY 61 RIHYVTVQKMPGOLPILEGVEFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHYVTVQKMPGOLPILEGVEFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 QY 121 KKTPTVLKATAGLRLLEHAKALLFEVKIFRSPFLVPKGSVINDGSDGILAWTV 180
 DB 121 KKTPTVLKATAGLRLLEHAKALLFEVKIFRSPFLVPKGSVINDGSDGILAWTV 180
 QY 181 NFLTGQLHGRHQETVGTGLDGGASTQITFLPQFEKLEQTPRGVLTGFEMFNSTYKLYTH 240
 DB 181 NFLTGQLHGRHQETVGTGLDGGASTQITFLPQFEKLEQTPRGVLTGFEMFNSTYKLYTH 240
 QY 241 SYLGFGGLKAARLATLGALETGTDGHTFRSACLPRWLEAWIFGGVKYQGGNQEVEGF 300
 DB 241 SYLGFGGLKAARLATLGALETGTDGHTFRSACLPRWLEAWIFGGVKYQGGNQEVEGF 300

Db 241 SYLGFGGLKAARLATLGALETGTDGHTFRSACLPRWLEAWIFGGVKYQGGNQEVEGF 300
 QY 301 EPCYAEVLRVVGRKLGHPQEEVQSGSFYAFSYYYDDRAVDTDMDYKGGILKVEDFERKAR 360
 Db 301 EPCYAEVLRVVGRKLGHPQEEVQSGSFYAFSYYYDDRAVDTDMDYKGGILKVEDFERKAR 360
 QY 361 EVCNDLENFTSGSPFFLCMDLSYITALLKDGFGPADSTVLQ 400
 Db 361 EVCNDLENFTSGSPFFLCMDLSYITALLKDGFGPADSTVLQ 400
 RESULT 9
 AAE19884
 ID AAE19884 standard; Protein; 465 AA.
 XX
 AC AAE19884;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Mouse CD39L4 protein.
 XX
 KW Mouse; CD-39-like protein; CD39L4 protein; therapy; immune deficiency;
 KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
 KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
 KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
 KW osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer;
 KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
 KW nervous system disease; nerve injury; ischaemia-reperfusion injury;
 KW endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
 KW Crohn's disease; virucide; antibacterial; antifungal; neuroprotective;
 KW dermatological; immunosuppressive; vulnerary; nontropic; anticonvulsant;
 KW antiinflammatory; nephrotropic; gastrointestinal; vasotropic; NTPase;
 KW nucleotide-triphosphatase; enzyme.
 XX
 OS Mus musculus.
 XX
 BN US6350447-B1.
 XX
 PD 26-FEB-2002.
 XX
 XX 29-JAN-1999; 99US-0240639.
 XX
 PR 29-JAN-1999; 99US-0240639.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Chadwick BP, Frischauf A;
 XX
 DR WPI; 2002-215262/27.
 DR N-PSDB; AAD31696.
 XX
 PT An isolated polypeptide with phosphohydrolase activity, designated
 PT CD39L2, useful to identify other proteins with which binding occurs or
 PT identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
 PT sclerosis and osteoporosis -
 XX
 XX Example; Fig 1; 101pp; English.
 PS
 CC The present invention relates to novel proteins with phosphohydrolase
 CC activity, designated CD-39-like (CD39L) proteins and polynucleotides
 CC encoding such proteins. CD39L proteins are useful to treat infectious
 CC diseases caused by viral, bacterial, fungal or other infection that may
 CC be treatable with CD39L. They are useful in the treatment of various
 CC immune deficiencies and disorders, autoimmune disorders such as multiple
 CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
 CC thyroiditis and insulin dependent diabetes mellitus, allergic reactions
 CC and conditions such as asthma and other respiratory problems, periodontal
 CC disease, osteoporosis, osteoarthritis and other tooth repair processes.
 CC They may have utility in compositions used for bone, cartilage, tendon,
 CC ligament and/or nerve tissue growth or regeneration as well as for wound
 CC healing and tissue repair and replacement and in the treatment of burns,
 CC incisions and ulcers. CD39L proteins may also be useful for proliferation
 CC of neural cells and for regeneration of nerve and brain tissue, i.e. for

the treatment of central nervous system diseases such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's disease, peripheral nervous system diseases peripheral nerve injuries, peripheral neuropathy and localised neuropathies. They are also used to treat mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. CD39L proteins of the invention are also useful to promote better or faster closure of non-healing wounds, including pressure ulcers, ulcers associated with vascular insufficiency and surgical and traumatic wounds. They also exhibit anti-inflammatory activity and may be used to treat inflammatory conditions including chronic or acute conditions, including ischaemia-reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease or Crohn's disease. The present sequence is mouse CD39L4 protein, also known as nucleotide-triphosphatase (NTPase).

Query Match 81.4%; Score 1832.5; DB 23; Length 465;
Best Local Similarity 83.8%; Pred. No. 6.8e-168;
Matches 352; Conservative 25; Mismatches 40; Indels 3; Gaps 3;
QY 1 MATSGTFFMLVSCVCSAYSHRNOQTFWFGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSGAV-FMLITACVGTTFVFEQQTWFGVFLSSMCPINVSAGTFYGMFDAGSTGA 59
QY 61 RIHVTVFKMPGQPLILEGEVFSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Db 60 RIHVTVFKTAGQLPFLBGIIFDSVKGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 119
QY 121 KKTVPVLKATGLRLPHKAKALLFEVKEIFRKSFFLVKGSVIMDGSDEGILAWTV 180
Db 120 ERTVPVLKATGLRLPHKAKALLFEVKEIFRKSFFLVKGSVIMDGSDEGILAWTV 179
QY 181 NFLTQGLHGRQETVGTLDLGASTQITFLPQFETKLEOTPRGYLTSPFEMNSTFKLYTH 240
Db 180 NFLTQGLHGRQETVGTLDLGASTQITFLPQFETKLEOTPRGYLTSPFEMNSTFKLYTH 239
QY 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGVKQYQGNQGEVGF 300
Db 240 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGVKQYQGNQGEVGF 299
QY 301 EPCYAEVLVRVKGKLPQEEVQVGSFYAFSYYYDRAVDTMIDYEKGLKVEDFERKAR 360
Db 300 EPCYAEVLVRVKGKLPQEEVQVGSFYAFSYYYDRAVDTMIDYEKGLKVEDFERKAR 359
QY 361 EVCDNLNFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKVNNIETGALGATPHL 420
Db 360 EVCDNLGSSFGSPFLCMDLYITALLKDGGLGFAERHPLTAHKE-SEQHRDW-LJLGGHL 417
RESULT 10
AAB53336
ID AAB53336 standard; Protein; 330 AA.
XX
AC AAB53336;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human colon cancer antigen protein sequence SEQ ID NO:876.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW identification; cytostatic; cardioactive; neuroprotective; vulnerable;
KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW nephrotropic; anti-infective; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
KW infectious disease; cardiovascular disorder.
XX
OS Homo sapiens.
XX
FN -WO200055351-A1.
XX

PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05883.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587534/55.
XX
DR N-PSDB; AAC98093.
XX
PT Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer -
XX
PS Claim 11; Page 1429-1431; 2104pp; English.
XX
CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC vulnerary, nephrotropic, anti-infective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins
CC may also be used to prevent diseases such as neural disorders, immune
CC gastrointestinal disorders, muscular disorders, reproductive disorders,
CC diseases, and cardiovascular disorders, wounds, renal disorders, infectious
CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
CC AAB54007 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 330 AA;
Query Match 73.8%; Score 1660; DB 21; Length 330;
Best Local Similarity 97.3%; Pred. No. 1.8e-151;
Matches 319; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 101 AETVQGLLEVAKOSIPRSHWKTFFVVKATAGLRLPHKAKALLFEVKEIFRKSFFLV 160
Db 3 ARAVQGLLEVAKOSIPRSHWKTFFVVKATAGLRLPHKAKALLFEVKEIFRKSFFLV 62
QY 161 KGSVIMDGSDEGILAWTVNFLTQGLHGRQETVGTLDLGASTQITFLPQFETKLEOT 220
Db 63 KGSVIMDGSDEGILAWTVNFLTQGLHGRQETVGTLDLGASTQITFLPQFETKLEOT 122
QY 221 PRGYLTSPFEMNSTFKLYTHSYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAE 280
Db 123 PXGYLTSPFEMNSTFKLYTHSYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAE 182
QY 281 WIFGVKQYQGNQGEVGFPCYAEVLVRVKGKLPQEEVQVGSFYAFSYYYDRAVDT 340
Db 183 WIFGVKQYQGNQGEVGFPCYAEVLVRVKGKLPQEEVQVGSFYAFSYYYDRAVDT 242
QY 341 MIDYEKGLKVEDFERKAREVCDNLNFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ 400
Db 243 MIDYEKGLKVEDFERKAREVCDNLNFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ 302
QY 401 LTKKVNNIETGALGATPHLQSLGISH 428
Db 303 LTKKVNNIETGALGATPHLQSLGISH 330
RESULT 11
AAE19881
ID AAE19881 standard; Protein; 456 AA.
XX
AC AAE19881;
XX

18-JUN-2002 (first entry)

Human CD39L2 protein.

Human; CD-39-like protein; CD39L2 protein; therapy; immune deficiency; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma; insulin dependent diabetes mellitus; periodontal disease; osteoporosis; osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer; Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease; nervous system disease; nerve injury; ischemia-reperfusion injury; endotoxin lethality; arthritis; nephritis; inflammation; bowel disease; Crohn's disease; virulence; antibacterial; antifungal; neuroprotective; dermatological; immunosuppressive; vulnerability; nootropic; anticonvulsant; antiinflammatory; nephrotropic; gastrointestinal; vasotropic.

Homo sapiens.

US6350447-B1.

26-FEB-2002.

29-JAN-1999; 99US-0240639.

29-JAN-1999; 99US-0240639.

(HYSE-) HYSEQ INC.

Chadwick BP, Frischauf A;

WPI; 2002-215262/27.

N-PSDB; AAD31693.

An isolated polypeptide with phosphohydrolase activity, designated CD39L2, useful to identify other proteins with which binding occurs or identify inhibitors and for treatment of, e.g., Alzheimer's, multiple sclerosis and osteoporosis.

Claim 1; Fig 4; 101pp; English.

The present invention relates to novel proteins with phosphohydrolase activity, designated CD-39-like (CD39L) proteins and polynucleotides encoding such proteins. CD39L proteins are useful to treat infectious diseases caused by viral, bacterial, fungal or other infection that may be treatable with CD39L. They are useful in the treatment of various immune deficiencies and disorders, autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune thyroiditis and insulin dependent diabetes mellitus, allergic reactions and conditions such as asthma and other respiratory problems, periodontal disease, osteoporosis, osteoarthritis and other tooth repair processes. They may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration as well as for wound healing and tissue repair and replacement and in the treatment of burns, incisions and ulcers. CD39L proteins may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central nervous system diseases such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's disease, peripheral nervous system diseases peripheral nerve injuries, peripheral neuropathy and localised neuropathies. They are also used to treat mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. CD39L proteins of the invention are also useful to promote better or faster closure of non-healing wounds, including pressure ulcers, ulcers associated with vascular insufficiency and surgical and traumatic wounds. They also exhibit anti-inflammatory activity and may be used to treat inflammatory conditions including chronic or acute conditions), including ischaemia-reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease or Crohn's disease. The present sequence is human CD39L2 protein.

Sequence 456 AA;

Query Match 44.4%; Score 999; DB 23; Length 456;

Best Local Similarity 52.4%; Pred. No. 2e-87;
Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;
QY 40 PINVSA---STLYGIMFDAGSTGTRTHVYTFVQKMPQQLPILSGEVPDSVKGGLSAFVDQ 96
Db 62 PLGTAADGHEVFGIMFDAGSTGTRVHVFOFT-RPPRETPTLTTHETPKAVKPGLSAYADD 120
QY 97 PKQGAETVOGLLEVAKDSDIPRSHWKKTPVVLKATAGLRLPEHKAKALLFEVKEIFRKP 156
Db 121 VESQAQGIREDLVAKQDIFDFWKATPLVLKATAGLRLPGEKAQKLLQKVKEVFKASP 180
QY 157 FLVPGKSVSMDGSDGILAWVTWFLTGOLHGHQBQTVGTLDLGGASTQITLPPQPEKT 216
Db 181 FLVGDGCVSTMNGTDEGVSAWITINFLTGLSKTPGGSSVGMVLDLGGGSGTQIAFLPRVEGT 240
QY 217 LEOTPGYLTSEFMENSTYKLYTHSYLGFGLKAARLATLGALETE-OTDCHTFRSACLPR 275
Db 241 LQASPPGYLTALRMFNRTYKLYSYLGLGMLMARLAILGGVGGQPKAKGKELVSPCLSP 300
QY 276 WLEAEMIFGGVYQYQGNQGEVGFEPFYAEVLVRVGRKLHQPEEVQVGRGFYAFSYYVDR 335
Db 301 SFGKEMEAHVTVRVSGQKAAASLHELCAARVSEVLQNRVHRTVEEVKHVDFYAFSYYVDL 360
QY 336 AVDTMDIDYEGKGLKVEDFERKAREVCONLENTSGSPFLCNDLSVITALLKDGFGFAD 395
Db 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCTRTLETQPOSSPFSCMDLTVVSLLOE-FGFP 419
QY 396 STVQLTKVNNIETGVALGATFHLQLSL 424
Db 420 SKVLLTRKIDNVETSWALGAIFHYIDSL 448

RESULT 12

AA072241

ID AAB72241 standard; Protein; 484 AA.

AC AAB72241;

XX 14-MAY-2001 (first entry)

XX Human CD39 like protein CD39-L2 amino acid sequence.

XX Human CD39-like protein; apyrase; NDase; platelet function inhibitor;

XX myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;

XX cerebral artery thrombosis; platelet aggregation; inflammation;

XX apoptosis; autoimmune disorder; neurological disorder;

XX Alzheimer's disease; Parkinson's disease; cancer; CD39-L2.

XX Homo sapiens.

XX WO200110205-A1.

XX 15-FEB-2001.

XX 09-AUG-2000; 2000WO-US21790.

XX 09-AUG-1999; 99US-0370265.

XX 11-JAN-2000; 2000US-0481238.

XX 25-APR-2000; 2000US-0557800.

XX 26-MAY-2000; 2000US-0583231.

XX 30-JUN-2000; 2000US-0608285.

XX (HYSE-) HYSEQ INC.

XX Ford J, Mulero JJ, Yeung G;

XX WPI; 2001-147489/15.

XX N-PSDB; AAF63386.

XX Polynucleotides encoding human CD39-like polypeptides, with apyrase and/or NDase activity, which are useful in the treatment of pathological conditions caused by thrombosis (e.g. myocardial infarction) and inflammatory disorders.

XX Claim 39; Page 162-164; 203pp; English.

XX This invention relates to polynucleotides encoding human CD39-like

CC polypeptides with apyrase and/or NTPase activity. The polypeptides having

CC ATPase, including NTPase, activity are useful for inhibiting platelet

CC function and can therefore be used in the prophylaxis or treatment of

CC pathological conditions caused by or involving thrombosis or excessive

CC coagulation or excessive platelet aggregation, such as myocardial

CC infarction, cerebral ischemia, angina, arterial thrombosis, cerebral

CC artery thrombosis or intracardiac thrombosis, and conditions associated

CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in

CC modulating disease states (including platelet aggregation, inflammation

CC and apoptosis) associated with ADP or other purinergic signalling by

CC reducing the levels of NTPs. The polypeptides are also useful for

CC prophylaxis or treatment of inflammation related disorders, such as

CC disorders involving sepsis or systemic inflammatory response syndrome or

CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,

CC cytokine overstimulation); autoimmune disorders such as thrombosis,

CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,

CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;

CC neurological disorders including neurodegenerative diseases, epilepsy,

CC depression, Alzheimer's disease, Parkinson's disease, Huntington's

CC disease, and amyotrophic lateral sclerosis; and cancer. The present

CC sequence represents human CD39 like protein CD39-L2.

XX Sequence 484 AA;

Query Match 44.4%; Score 999; DB 22; Length 484;

Best Local Similarity 52.4%; Pred. No. 2.2e-87;

Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;

QY 40 PINVSA---STLYGIMFDAGSTGTRIHYVTFVQKMPQLPILGEGVDSVKPGLSAFVDQ 96

DB 90 PLGTAADGHEVFGIMFDAGSTGTRVHVQFT-RPREPTTLTHETFKALPKGLSAYADD 148

QY 97 PKQAGTVOGLLEVAKDSIPRSHWKTTPVLKATAGLRLPPEHKAALLFEVKEIFRKPSP 156

DB 149 VEKSAQGIKRELLDVAQKQIDPFDFWKATPLVLRATAGLRLPPEHKAALLFEVKEIFRKPSP 208

QY 157 FLVPGKGSVIMDSDEGILAWTVNFLTQHLGHRQETVGTDLGGASTQITFLPQPEKT 216

DB 209 FLVGDCCVIMNGTDEGVSAMITINFLTQSLTKPGSSVGMGLDGGSTQITFLPQPEKT 268

QY 217 LQTPRGYLTSPFEMNSTYKLYTHSYVGLGPKAARLATLGALETE-GTDGHTFRACALPR 275

DB 269 LQASPPGYLTALRMENRTYKLYSYVGLGPKAARLATLGALETE-GTDGHTFRACALPR 328

QY 276 WLEAEWIFCGYKQYGGNDEGEVGFPCVAEVLVRVGRKHLQHPBEVQRGSFVAFYYDR 335

DB 329 SPFGMEHAEVTVYRVSQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFVAFYYIDL 388

QY 336 AVDTMDIDYKGGILKVEDFERKAREVCNLENFTSGSPFLCNDLSYITALLKDGFGAD 395

DB 389 AGVGLIDAEKGGSLVGVGFETAAKVCTLTQTQSSPFSFSCMDLTYVSLLLQE-FGPR 447

QY 396 STVLOLTQKVNINFTGALGFHLLQSL 424

DB 448 SKVLKTRKIDNVETSWALGAFHVIDSL 476

RESULT 13

ABB06124

ID ABB06124 standard; Protein; 463 AA.

XX ABB06124;

XX ABB06124;

DT 10-MAY-2002 (first entry)

XX Human NS protein sequence SEQ ID NO:216.

DE Human; cytostatic; osteopathic; gynaecological; neuroprotective;

KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;

KW vasotropic; antiarteriosclerotic; antiinflammatory; cardiovascular; dermatological;

KW anorectic; muscular; antiinfertility; cardiovascular; anticoagulant;

KW antifibrinolytic; hypotension; antidiabetic; immunomodulator; cardiac;

KW anticonvulsant; antidiabetic; tranquilizer; antidepressant; antiepileptic;

KW gastrointestinal; virucide; antiulcer; cerebroprotective; nootropic;

KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;

KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;

KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;

KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;

KW infertility; cardiovascular disease; coagulation disease; hypertension;

KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;

KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;

XX gastric ulcer; Alzheimer's disease.

OS Homo sapiens.

XX WO200206315-A2.

XX 24-JAN-2002.

XX 17-JUL-2001; 2001WO-IL00653.

PR 18-JUL-2000; 2000IL-0137345.

PR 15-DEC-2000; 2000IL-0140354.

XX (COMP-) COMPUGEN LTD.

PI Mintz L, Freilich S, Bernstein J;

XX WP1; 2002-155037/20.

DR N-PSDB; ABL39778.

XX One hundred and twenty eight novel nucleic acid sequences, useful for

XX creating and diagnosing e.g. cancer, asthma and Alzheimer's.

PS Claim 6; Page 251-253; 290pp; English.

XX ABL39691 to ABL39818 represent novel human nucleic acid sequences

XX encoding the proteins given in ABB06037 to ABB06164. The novel sequences

XX (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,

XX antirheumatic, antipsoriatic, antiepileptic, ophthalmological, virucide,

XX vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,

XX anorectic, muscular, anti-HIV, antiinfertility, cardiovascular,

XX anticonvulsant, antifibrinolytic, hypotension, antidiabetic, cardiac,

XX immunomodulator, anticonvulsant, antidiabetic, tranquilizer, antiulcer,

XX antidepressant, gastrointestinal, antiepileptic, cerebroprotective,

XX nootropic and contraceptive activities. The NS can be used in vaccines,

XX gene therapy and antitense therapy. Nucleic acids, expression vectors and

XX antibodies from the present invention can be used for treating and

XX diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative

XX diseases, dystonia, multiple sclerosis, inflammation, skin disorders,

XX cataracts, restenosis, atherosclerosis, rheumatoid arthritis, psoriasis,

XX glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular

XX disease, coagulation disease, ischaemia, hypertension, asthma, immune

XX depression, epilepsy, angina, neurodegeneration, diabetes, anxiety,

XX depression, schizophrenia, viral disease, gastric ulcers, stroke,

XX Alzheimer's disease and as a contraceptive.

Sequence 463 AA;

Query Match 44.3%; Score 996; DB 23; Length 463;

Best Local Similarity 52.2%; Pred. No. 4e-87;

Matches 203; Conservative 57; Mismatches 123; Indels 6; Gaps 4;

QY 40 PINVSA---STLYGIMFDAGSTGTRIHYVTFVQKMPQLPILGEGVDSVKPGLSAFVDQ 96

DB 90 PLGTAADGHEVFGIMFDAGSTGTRVHVQFT-RPREPTTLTHETFKALPKGLSAYADD 127

QY 97 PKQAGTVOGLLEVAKDSIPRSHWKTTPVLKATAGLRLPPEHKAALLFEVKEIFRKPSP 156

DB 128 VEKSAQGIKRELLDVAQKQIDPFDFWKATPLVLRATAGLRLPPEHKAALLFEVKEIFRKPSP 187

QY 157 FLVPGKGSVIMDSDEGILAWTVNFLTQHLGHRQETVGTDLGGASTQITFLPQPEKT 216

Db 188 FLVGDDCVSMNGTDEGVSAMITNFTLSKLTGSSVGMGLDGGSGTQIAFLPRVEGT 247
 QY 217 LEOTPRGVLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTGDHTFRSACLPR 275
 Db 248 LQASPPGYLTALRMFNRTYKLYSYLGGLMSARLAILGVGEQPAKDKELVSPCLSP 307
 QY 276 WLEAEWIFGGVYQYGNQGEVGFPCYAEVLVRVVKLHQPEVQVGSFYAFSYYDDR 335
 Db 308 SFKGEWEHAEVTVRSVQKAAASLHELCAARVSEVLQNRVHRTVEVXVDFYAFSYYDL 367
 QY 336 AVDTMDIDYKGGILKVEDFERKAREVCDNLNFTSGSPFLCWDLSYITALLKDGFGAD 395
 Db 368 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRITLQPSPPSCMDLTYSVLLQOE-FGFP 426
 QY 396 STVLQTKKNNIETGVALGATFHLLQSL 424
 Db 427 SKVLKLRKIDNVETSWALGAIFHYIDSL 455

RESULT 14
 ABJ04657
 ID ABJ04657 standard; Protein: 467 AA.
 AC ABJ04657;
 XX
 DT 11-OCT-2002 (first entry)
 XX
 DE Protein of NOVX 15a SEQ ID No 36.
 XX
 KW Cytostatic; antidiabetic; anorectic; metabolic; nootropic; antilipaeamic;
 KW neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective;
 KW tranquiliser; neuroleptic; antidiabetic; antiulcer; antiinflammatory;
 KW anti-HIV; antiallergic; antirheumatic; antiarthritic; NOVX; diabetes;
 KW metabolic disorder; obesity; infectious disease; Alzheimer's disease;
 KW anorexia; neurodegenerative disorder; Parkinson's disorder; obesity;
 KW immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease;
 KW metabolic syndrome X; wasting disorder; cancer; neurological disorder;
 KW epilepsy; stroke; mental disorder; schizophrenia; disorders; goiter;
 KW vesicular transport; cystic fibrosis; gastrointestinal disorder;
 KW diabetes mellitus; ulcerative colitis; AIDS; allergic reaction;
 KW multiple sclerosis; rheumatoid arthritis; transgenic animal;
 KW Gene therapy.
 XX
 OS Unidentified.
 XX
 PN W0200246409-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 06-DEC-2001; 2001WO-US46586.
 XX
 PR 06-DEC-2000; 2000US-251660P.
 PR 12-DEC-2000; 2000US-255029P.
 PR 08-JAN-2001; 2001US-260326P.
 PR 24-JAN-2001; 2001US-263800P.
 PR 20-FEB-2001; 2001US-269942P.
 PR 24-APR-2001; 2001US-286183P.
 PR 20-AUG-2001; 2001US-313627P.
 PR 12-SEP-2001; 2001US-318712P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Guo X, Li L, Patuturajan M, Shimkets RA, Casman SJ, Malyanhar UM;
 PI Tchernev VT, Vernet CM, Spytek KA, Shenoy SG, Alsobrook JP;
 PI Edinger S, Peyman JA, Stone DJ, Eilerman K, Gangolli EA;
 PI Boldog FL, Colman SD, Eisen AJ, Liu X, Padigaru M, Spaderna SK;
 PI Zerhusen BD;
 XX
 DR WPI: 2002-547774/58.
 DR N-PSDE; ABT05470.
 XX
 DT Novel isolated polypeptide, designated NOVX, useful for treating or

PT preventing cancer, diabetes, obesity, dyslipidemia, anorexia, and
 XX metabolic, neurodegenerative, immune and hematopoietic disorders
 XX
 XX Claim 1; Page 140; 421pp; English.
 CC The invention relates to an isolated polypeptide, designated NOVX,
 CC comprising a sequence fully defined in the specification. The isolated
 CC protein, its encoding polynucleotide or an antibody created from the
 CC protein is useful in the manufacture of a medicament for treating a
 CC syndrome associated with a human disease, preferably a NOVX-associated
 CC disorder, or for treating or preventing a NOVX-associated disorder in a
 CC subject, preferably human. The isolated protein, its encoding
 CC polynucleotide or an antibody created from the protein are also useful
 CC for treating or preventing metabolic disorders, diabetes, obesity,
 CC infectious disease, anorexia, neurodegenerative disorder, Alzheimer's
 CC disease, Parkinson's disorder, immune disorders, haematopoietic
 CC disorders, and various dyslipidaemias, metabolic disturbances associated
 CC with obesity, the metabolic syndrome X, wasting disorders associated with
 CC chronic diseases, and cancer. The isolated protein, its encoding
 CC polynucleotide or an antibody created from the protein are useful for
 CC treating or preventing neurological disorders such as epilepsy, stroke,
 CC mental disorders including mood, anxiety, schizophrenic disorders,
 CC disorders of vesicular transport such as cystic fibrosis, diabetes
 CC mellitus, goiter, gastrointestinal disorders including ulcerative
 CC colitis, other conditions associated with abnormal vesicle trafficking
 CC including AIDS, allergic reactions, multiple sclerosis and rheumatoid
 CC arthritis. A cell comprising the vector of the invention is useful for
 CC producing non-human transgenic animals. The polynucleotide of the
 CC invention can be used to treat disorders by gene therapy. This sequence
 CC represents one of the isolated NOVX proteins of the invention.

XX Sequence 467 AA;

Query Match 44.3%; Score 996; DB 23; Length 467;
 Best Local Similarity 52.2%; Pred. No. 4e-87;
 Matches -203; Conservative 57; Mismatches 123; Indels 6; Gaps 4;
 QY 40 PINVSA---STLYGIMFDAGSTGRTHVTVTFVQMPGQLPILGEVDSVKPGLSAFVDQ 96
 Db 73 PLGTAADGHEVFGYIMFDAGSTGRVHVQFT-RPPRETPTLTHTFKALPKGLSAYADD 131
 QY 97 PQGAEVTVQGLLEAVKDSIPRSHKKTTPVVLKATAGLRLLPEHKAKALLFEVKEIFRSP 156
 Db 132 VEKSAQGIREDLDVAQKQDIPDFFWKATPLVLKATAGLRLLPEKAKQLQKVEFKASP 191
 QY 157 FLVPKGSVIMDGSDEGILAVTVNFLTQGLHGRQETVGLDLGGASTQITFLPQFEKT 216
 Db 192 FLVGDDCVSMNGTDEGVSAMITNFTLSKLTGSSVGMGLDGGSGTQIAFLPRVEGT 251
 QY 217 LSQTPRGYLTSPFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTGDHTFRSACLPR 275
 Db 252 LQASPPGYLTALRMFNRTYKLYSYLGGLMSARLAILGVGEQPAKDKELVSPCLSP 311
 QY 276 WLEAEWIFGGVYQYGNQGEVGFPCYAEVLVRVVKLHQPEVQVGSFYAFSYYDDR 335
 Db 312 SFKGEWEHAEVTVRSVQKAAASLHELCAARVSEVLQNRVHRTVEVXVDFYAFSYYDL 371
 QY 336 AVDTMDIDYKGGILKVEDFERKAREVCDNLNFTSGSPFLCWDLSYITALLKDGFGAD 395
 Db 372 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRITLQPSPPSCMDLTYSVLLQOE-FGFP 430
 QY 396 STVLQTKKNNIETGVALGATFHLLQSL 424
 Db 431 SKVLKLRKIDNVETSWALGAIFHYIDSL 459

RESULT 15
 AAM93929
 ID AAM93929 standard; Protein: 456 AA.
 XX
 AC AAM93929;
 XX
 DT 06-NOV-2001 (first entry)

